

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: January 15, 2005, 15:01:47 ; Search time 2260 Seconds  
(without alignments)  
9332.392 Million cell updates/sec

Title: US-10-009-579-5\_COPY\_3115\_3560  
Perfect score: 446  
Sequence: 1 gtaatggcacatctctgt.....ctggaaggttctgcctgt 446

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 90534458

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing First 45 summaries

Database : GenEmbl:  
1: gb\_ba:\*
2: gb\_htg:\*
3: gb\_in:\*
4: gb\_on:\*
5: gb\_ov:\*
6: gbDat:\*
7: gb\_Dh:\*
8: gb\_Pi:\*
9: gb\_pr:\*
10: gb\_ro:\*
11: gb\_sts:\*
12: gb\_sy:\*
13: gb\_un:\*
14: gb\_v1:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	446	100.0	4069	9 AY148099	AY148099 Homo sapi
2	446	100.0	4282	6 AX254778	AX254778 Sequence
3	446	100.0	17197	9 AC079775	AC079775 Homo sapi
C 4	173.4	38.9	97288	9 AL356055	AL356055 Human DNA
C 5	172.2	38.6	110130	9 AL360268	AL360268 Human DNA
C 6	171.6	38.5	58723	9 AL391237	AL391237 Human DNA
C 7	171.4	38.4	158405	9 AC021763	AC021763 Homo sapi
8	171.4	38.4	187200	2 AP001379	AP001379 Homo sapi
9	171	38.3	69829	9 AC064841	AC064841 Homo sapi
C 10	171	38.3	178670	2 AC009290	AC009290 Homo sapi
C 11	170.6	38.3	176075	9 AC017079	AC017079 Homo sapi
C 12	170	38.1	568	6 AX871940	AX871940 Sequence
C 13	170	38.1	568	6 BD152002	BD152002 Primer fo
C 14	170	38.1	163593	9 AC144522	AC144522 Homo sapi
C 15	170	38.1	165593	2 AC026856	AC026856 Homo sapi
C 16	169.6	38.0	66266	2 AP000573	AP000573 Homo sapi
C 17	169.6	38.0	77265	2 AC099810	AC099810 Homo sapi
C 18	169.6	38.0	1663356	9 AP001453	AP001453 Homo sapi
C 19	169.6	38.0	174562	2 AC005848	AC005848 Homo sapi

## ALIGNMENTS

RESULT 1  
AY148099  
LOCUS AY148099 4169 bp DNA linear  
DEFINITION Homo sapiens EGFP (TACSTD1) gene, promoter region and 5' UTR.  
ACCESSION AY148099  
VERSION AY148099.1 GI:24935271  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 4069)  
AUTHORS McLaughlin, P.M.J., Trpis, M., Kroesen, B.-J., Helfrich, W.,  
Terpstra, P., Rutgers, M.H.C., de Leij, L.F.M.H. and Harmsen, M.C.  
TITLE Use of the EGFP-2 promoter for targeted expression of heterologous  
genes in carcinoma-derived cell lines  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 4069)  
AUTHORS McLaughlin, P.M.J., Trpis, M., Kroesen, B.-J., Helfrich, W.,  
Terpstra, P., Rutgers, M.H.C., de Leij, L.F.M.H. and Harmsen, M.C.  
TITLE Direct Submission  
JOURNAL Hanzeplein 1, Groningen 913GZ, The Netherlands  
FEATURES Source  
SUBMITTED (04-SEP-2002) PathLabMed-Mol-Biol, University Groningen,  
Location/Qualifiers 1. .4069  
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/db\_xref="taxon:9606"  
/chromosome="12"  
/map="3p16.3"  
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/gene="TACSTD1"  
/note="synonyms: EGP2, GA733-2"  
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3975..>4069  
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/product="EGP2"  
/note="putative transcription start"  
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/gene="TACSTD1"  
/origin 5'UTR

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Qy	1	GTATGGACGAACTCTGTCAGTCAACCTCAGCCCTCCAGTAGCTGGATTACAGC 60						
Db	3112	GTATGGACGAACTCTGTCAGTCAACCTCAGCCCTCCAGTAGCTGGATTACAGC 3171						
Qy	61	ATCGGCCAACCGCCGGTAATTGTATCTTGTATTTGTATCTTGTATCTCCATGTT 120						
Db	3172	ATCGGCCAACCGCCGGTAATTGTATCTTGTATCTTGTATCTCCATGTT 3231						
Qy	121	GCTCAGGCTACGCCGGTAACTCAACACTCGGTGATCGCCCGCTCGACCTCCAAAGT 180						
Db	3232	GCTCAGGCTACGCCGGTAACTCAACACTCGGTGATCGCCCGCTCGACCTCCAAAGT 3291						
Qy	181	GCTAGGTTAAGGCCAGGCTTACACCTTGCTGAGCTTACATCTTC 240						
Db	3292	GCTAGGTTAAGGCCAGGCTTACACCTTGCTGAGCTTACATCTTC 3351						
Qy	241	AAGTGTCTGAAATGCTTATGAACGAAAAAGGTTATAAGGTAAATTATAAGAAC 300						
Db	3352	AAGTGTCTGAAATGCTTATGAACGAAAAAGGTTATAAGGTAAATTATAAGAAC 3411						
Qy	301	ACATCATTTCTCCCAAGAGGCCAGATTCTTCTCTCTCTCTCTCTCTCTCTCT 360						
Db	3412	ACATCATTTCTCCCAAGAGGCCAGATTCTTCTCTCTCTCTCTCTCTCTCTCT 3471						
Qy	361	TTCCTAATTCTAGGAGTATAATTAAATTGCAGGTAAGCTCAAGGCTCTTTAT 420						
Db	3472	TTCCTAATTCTAGGAGTATAATTGCAGGTAAGCTCAAGGCTCTTTAT 3531						
Qy	421	AGTGTCTGGAAAGGTTCTGCCCTG 446						
Db	3532	AGTGTCTGGAAAGGTTCTGCCCTG 3557						
RESULT 3								
		AC079775	AC079775	AC079775	AC079775	AC079775	AC079775	AC079775
LOCUS		LOCUS	LOCUS	LOCUS	LOCUS	LOCUS	LOCUS	LOCUS
DEFINITION		Homo sapiens BAC clone RP11-295P2	from 2,	complete	sequence.	PRI 29-MAY-2002		
ACCESSION		AC079775	AC079775	AC079775	AC079775	AC079775	AC079775	AC079775
VERSION		1	1	1	1	1	1	1
KEYWORDS		HTG.						
ORGANISM		Homo sapiens (human)						
SOURCE		Homo sapiens						
REFERENCE		Belter,E., Haakenson,W., Doepper,A. and Elliott,G.						
AUTHORS		The sequence of Homo sapiens BAC clone RP11-295P2						
JOURNAL		Unpublished (2001)						
TITLE		1 (bases 1 to 171987)						
MEDLINE		3 (bases 1 to 171987)						
PUBLMED		5 (bases 1 to 171987)						
AUTHORS		Sulston,J.E. and Waterston,R.						
JOURNAL		Toward a complete human genome sequence						
TITLE		Genome Res. 8 (11), 1097-1108 (1998)						
MEDLINE		99631792						
PUBLMED		9847074						
AUTHORS		Waterston,R.H.						
JOURNAL		4 (bases 1 to 171987)						
REFERENCE		Waterston,R.H.						
AUTHORS		Direct Submission						
JOURNAL		Submitted (30-MAR-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108 USA						
REFERENCE		5 (bases 1 to 171987)						
AUTHORS		Waterston,R.H.						
JOURNAL		Direct Submission						
COMMENT		Submitted (30-MAR-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108 USA						
FEATURES		5 (bases 1 to 171987)						
source		Waterston,R.H.						
ORIGIN		Direct Submission						
Query Match	100.0%	Score 446;	DB 6;	Length 4282;				
Best Local Similarity	100.0%	Pred. No. 3 .5e-96;						
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Db	3115	GTATGGACGAACTCTGTCAGTCAACCTCAGCCCTCCAGTAGCTGGATTACAGC 3174						
ORIGIN								
Query Match	100.0%	Score 446;	DB 6;	Length 4282;				
Best Local Similarity	100.0%	Pred. No. 3 .5e-96;						
Matches 446;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;				
Qy	1	GTATGGACGAACTCTGTCAGTCAACCTCAGCCCTCCAGTAGCTGGATTACAGC 60						
Db	3115	GTATGGACGAACTCTGTCAGTCAACCTCAGCCCTCCAGTAGCTGGATTACAGC 120						



only a small overlap as described above.	
This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sv:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at:	
<a href="http://www.sanger.ac.uk/Projects/C_elegans/wormpep">http://www.sanger.ac.uk/Projects/C_elegans/wormpep</a> This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at <a href="http://www.sanger.ac.uk/HGP/Chr1">http://www.sanger.ac.uk/HGP/Chr1</a>	
RPL1-41A14 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see <a href="http://www.chori.org/bacpac/home.htm">http://www.chori.org/bacpac/home.htm</a>	
FEATURES	
source	Location/Qualifiers
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	/mol_type="genomic DNA"
	/db_xref="taxon:9606"
	/chromosome="1"
	/clone="RP11-41A14"
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Query Match	38.9%
Best Local Similarity	87.9%
Matches	189;
Conservative	0;
	Pred. No. 7.8e-31;
	Indels 0;
	Gaps 0;
	0;
Qy	1
Db	78382
Qy	61
Db	78322
Qy	121
Db	78262
Qy	181
Db	78202
RESULT 5	
AL360268/c	AL360268
DEFINITION	Human DNA sequence from clone RP11-379C10 on chromosome 9, complete sequence.
ACCESSION	AL360268
VERSION	AL360268.14
KEYWORDS	GI:19351891
SOURCE	HTG.
Homo sapiens (human)	
Lloyd, D	(bases 1 to 110130)
ORGANISM	
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
COMMENT	Submitted (09-MAR-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridge, UK. 100 1SA, UK. E-mail enquiries: <a href="mailto:clonerquest@sanger.ac.uk">clonerquest@sanger.ac.uk</a> Clone requests: <a href="mailto:hungry@sanger.ac.uk">hungry@sanger.ac.uk</a> On Mar 11, 2002 this sequence version replaced gi:186506822. During sequence assembly data is compared from overlapping clones. When differences are found these are annotated as variations.

together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. This sequence was finished unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL:, Sw:, SWISSPROT:, Tr:, TREMBL:, Wp:, WORMPEP:, Information on the WORMPEP database can be found at [http://www.sanger.ac.uk/Projects/C\\_elegans/wormpep](http://www.sanger.ac.uk/Projects/C_elegans/wormpep). This sequence was generated from part of bacterial clone contigs of human chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr9>. RP11-379C10 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm>

## FEATURES

## Source

1. .110130  
*/organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"  
 /chromosome="19"  
 /clone="RP11-379C10"  
 /clone\_lib="RPCI-11.2"*  
 misc\_feature 64768 \_  
*/note="Tandem repeat. Forced join. Gap size estimated to be approximately 200bp by restriction digest data."*

## ORIGIN

Query Match 38.6%; Score 172.2; DB 9; Length 110130;  
 Best Local Similarity 87.3%; Pred. No. 1.5e-30;  
 Matches 200; Conservate 0; Mismatches 28; Indels 1; Gaps 1;  
 Source  
 Qy 1 GAAATGCACTGGCCGGTAATTGTGTTAGTAGAGACGGGTCTCCATGTT  
 Db 74369 GCAATGCATGATCGCTGCTACTGTGCTCCATGTT 74251  
 Qy 61 ATGGCCACCACTGGCCGGTAATTGTGTTAGTAGAGACGGGTCTCCATGTT 120  
 Db 74250 GGTCAGGTGGTCTGAACACTGTGCTCCATGTT 74191  
 Qy 121 GCTAGGATTACAGGGTGAGCCACGGTCAACCTCAAGCTT 229  
 Db 74190 GCTGGGATTACAGGGTGAGCCACGGTCAACCTCAAGCTT 74142  
 CDS  
 RESULT 6 AL391237/  
 LOCUS AL391237 Human DNA sequence from clone RP11-125M24 on chromosome Xq23-25  
 DEFINITION Contains part of the gene for KIAA1058 protein, an EST, an SRS and GS3s, complete sequence.  
 ACCESSION AL391237  
 VERSION GI:12057239

KEYWORDS HTG; KIAA1058.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 REFERENCE 1. (bases 1 to 58723)  
 AUTHORS Wilson,S.  
 TITLE Direct Submission  
 JOURNAL Submitted (26-MR-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk  
 COMMENTS requests: cloner@sanger.ac.uk  
 On Jan 9, 2001 this sequence version replaced 9i:10716346. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variants together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL:, Sw:, SWISSPROT:, Tr:, TREMBL:, Wp:, WORMPEP:, Information on the WORMPEP database can be found at [http://www.sanger.ac.uk/Projects/C\\_elegans/wormpep](http://www.sanger.ac.uk/Projects/C_elegans/wormpep). This sequence was generated from part of bacterial clone contigs of human chromosome X, constructed by the Sanger Centre Chromosome X Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/ChrX>.  
**IMPORTANT:** This sequence is not the entire insert of clone RP11-125M24. It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true right end of clone RP13-12804 is at 26135 in this sequence. The true left end of clone RP6-155F9 is at 100 in this sequence. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. RP11-125M24 is from the library RPCI-13.1 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm>

FEATURES

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 /db\_xref="taxon:9606"  
 /chromosome="19"  
 /clone="RP11-379C10"  
 /clone\_lib="RPCI-11.2"*  
 misc\_feature 64768 \_  
*/note="Tandem repeat. Forced join. Gap size estimated to be approximately 200bp by restriction digest data."*

Location/Qualifiers

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 gene 10479..1509  
*/note="match: GSS: Em:AQ110399"  
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/evidence=not experimental
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repeat_region .4691. .5493 .note="12 repeat: matches 5342. .6144 of consensus"
repeat_region .6498. .6849 .note="THE1A repeat: matches 1. .354 of consensus"
repeat_region .7361. .7390 .note="12 repeat: matches 2681. .2710 of consensus"
repeat_region .7391. .7617 .note="MER16A repeat: matches 1. .236 of consensus"
repeat_region .7618. .8526 .note="12 repeat: matches 1710. .2681 of consensus"
repeat_region .8904. .9133 .note="11MBS repeat: matches 5940. .6169 of consensus"
repeat_region .11296. .11457 .note="PRAK repeat: matches 2. .161 of consensus"
repeat_region .11516. .11598 .note="MIR repeat: matches 23. .197 of consensus"
repeat_region .12983. .13173 .note="MER repeat: matches 3. .215 of consensus"
repeat_region .13174. .13485 .note="Alus repeat: matches 1. .308 of consensus"
repeat_region .13486. .13517 .note="MIR repeat: matches 215. .243 of consensus"
repeat_region .13511. .13511 .note="12 repeat: matches 2055. .2748 of consensus"
repeat_region .14190. .14492 .note="MER repeat: matches 1. .305 of consensus"
repeat_region .14821. .15137 .note="AlusX repeat: matches 1. .305 of consensus"
repeat_region .15162. .15241 .note="MER repeat: matches 58. .140 of consensus"
repeat_region .15318. .15477 .note="12 repeat: matches 2570. .2746 of consensus"
repeat_region .15595. .15688 .note="AlusX repeat: matches 1. .294 of consensus"
repeat_region .15911. .16504 .note="12 repeat: matches 2080. .2710 of consensus"
repeat_region .16880. .16837 .note="MER20 repeat: matches 2326. .2384 of consensus"
repeat_region .17031. .17241 .note="MER20 repeat: matches 1. .218 of consensus"
repeat_region .17467. .17566 .note="12 repeat: matches 2594. .2698 of consensus"
repeat_region .17560. .17597 .note="# copies 2 mer tt 89% conserved"
repeat_region .17570. .17597 .note="# copies 2 mer tt 100% conserved"
repeat_region .18437. .18593 .note="MER3 repeat: matches 2472. .3053 of consensus"
repeat_region .19010. .19129 .note="MER3 repeat: matches 9. .166 of consensus"
repeat_region .19130. .19413

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RESULT 7	AC021763/c	AC021763	158405 bp	DNA linear	PRI 23-AUG-2002		Roy,A., Schauer,S., Schupback,R., Seaman,S., Severy,P., Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
LOCUS	Homo sapiens chromosome 18, clone RP1-56021, complete sequence.						
DEFINITION							
ACCESSION	AC021763						
VERSION	AC021763.10						
VERSION	GI:22450664						
KEYWORDS	HTG,						
SOURCE	Homo sapiens (human)						
ORGANISM	Homo sapiens						
AUTHORS	Birren,B., Nusbaum,C. and Lander,E.						
REFERENCE							
TITLE	Homo sapiens chromosome 18, clone RP1-56021						
JOURNAL	Unpublished						
REFERENCE	2 (bases 1 to 158405)						
AUTHORS	Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., Anderson,S., Baldwin,J., Barna,N., Beckery,R., Beda,F., Boguslavskiy,L., Boukhgalter,B., Burket,G., Castle,A., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P., Dearlano,K., Dewar,K., Domino,M., Doyle,M., Fenster,J., Ferreira,P., Fitzhugh,W., Forrest,C., Gage,D., Galagan,J., Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L., Howland,J.C., Johnson,R., Jones,C., Kann,L., Kartas,A., Klein,J., Landers,T., Lehozky,J., Levine,C., Liu,G., Locke,K., Macdonald,P., Marcus,N., McEwan,P., McGurk,A., McKernan,K., McPheeters,R., Meldrim,J., Menuez,J., Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P., Olivari,T.M., Peterson,K., Pierre,N., Pisani,C., Pollara,V., Raymond,C., Riley,R., Rotman,D., Roy,A., Santos,R., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Tirrell,A., Vassiliev,H., Viel,R., Vo,A., Wu,X., Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.						
TITLE	Submitted (20-JAN-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA						
REFERENCE	3 (bases 1 to 158405)						
AUTHORS	Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavskiy,L., Boukhgalter,B., Canarate,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A., Cook,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., Fitzgerald,M., Gage,D., Galagan,J., Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kann,A., Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K., Liu,G., Maclean,C., Macdonald,P., Major,J., Matthews,C., McCarthy,M., Melidim,J., Menuez,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K., Phankhang,P., Pierre,N., Raymond,C., Rettig,R., Riise,C., Rogov,P., Roman,J., Roy,A., Schauer,S., Schupback,R., Seaman,S., Severy,P., Smith,C., Spender,B., Stange-Thomann,N., Stojanovic,N., Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.						
JOURNAL	Submitted (06-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA						
REFERENCE	4 (bases 1 to 158405)						
AUTHORS	Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavskiy,L., Boukhgalter,B., Canarate,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A., Cook,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., Fitzgerald,M., Gage,D., Galagan,J., Hagos,B., Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kann,A., Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K., Liu,G., Maclean,C., Macdonald,P., Major,J., Matthews,C., McCarthy,M., Meldrim,J., Menuez,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K., Phankhang,P., Pierre,N., Raymond,C., Rettig,R., Riise,C., Rogov,P.,						

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Qy 181 GCTAGGATTACGGGTGAGCCACGGCTCAGCTGGAAACCTTGCTTACAGTC 237  
Db 19216 GCTGGATTACCGTAGCCACTGCAACTCTAGCTGGATAGCTGGATTACAGGC 19160

RESULT 8 AP001379 LOCUS AP001379 187200 bp DNA linear HTG 15-JUL-2000 DEFINITION Homo sapiens chromosome 18 clone RP1-850H3 map 18q12, WORKING DRAFT SEQUENCE, 21 unordered pieces.

ACCESSION AP001379 VERSION AP001379.3 GT:9229958 KEYWORDS HTGS PHASE1; HTGS\_DRAFT. SOURCE Homo sapiens (human)

ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 187200)  
AUTHORS Hattori,M., Ishii,K., Toyota,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.

TITLE Homo sapiens 187,200 Genomic DNA of 18q12  
JOURNAL Published Only in DataBase (2000)  
AUTHORS Hattori,M., Ishii,K., Toyota,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.

JOURNAL Direct Submission  
TITLE Submitted (09-MAR-2000) Masahiro Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);  
1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555, Japan  
(E-mail:hattori@gsc.riken.go.jp, URL:http://hgcp.gsc.riken.go.jp/, Tel:81-42-778-9923, Fax:81-42-778-9924)  
COMMENT On Jul 15, 2000 this sequence version replaced gi:8117292.  
JOURNAL Genome Center  
CENTER RIKEN Genomic Sciences Center (GSC)  
Center code: RIKEN  
Web site: http://hgcp.gsc.riken.go.jp/  
Contact: hattori@gsc.riken.go.jp/  
----- Project Information  
Center project name: HumanDraft18  
Center clone name: RP1-850H3  
----- Summary Statistics  
Sequencing vector: PCR products; 100% of reads  
Chemistry: Dye-terminator  
Assembly program: Phrap; version 0.990329  
Consensus quality: 179/71 bases at least Q40  
Consensus quality: 182/832 bases at least Q30  
Consensus quality: 184/194 bases at least Q20  
Insert size: 185200, sum-of-contigs  
Quality coverage: 9.46x in Q20 bases, sum-of-contigs  
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NOTE: This is a 'working draft' sequence. It currently consists of 21 contigs. The true order of the sequence is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

33581 contig of 33581 bp in length  
1 33682 58093 contig of 24412 bp in length  
58194 77675 contig of 19432 bp in length  
77726 97031 contig of 19306 bp in length  
97132 111930 contig of 14859 bp in length  
112091 125455 contig of 13375 bp in length  
125566 135454 contig of 9898 bp in length  
135555 144628 contig of 9074 bp in length  
144729 151062 contig of 6334 bp in length  
151163 155511 contig of 4349 bp in length  
155612 160186 contig of 4575 bp in length  
160287 164088 contig of 3802 bp in length  
161489 167739 contig of 3551 bp in length  
167840 171188 contig of 3349 bp in length  
174981 contig of 3693 bp in length

Query Match 38.4%; Score 171.4; DB 9; Length 158405;  
Best Local Similarity 82.7%; Pred. No. 2.5e-30;  
Matches 196; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

1 GTANTGGCACGATCTCTGTACTGCAACTCTAGCTGGATAGCTGGATTACAGGC 60  
Db 19396 GCAGTGGCTGATCTCAGTCACGGCAACTCTAGCTGGATAGCTGGATTACAGGC 19337  
61 ATGGCCCAACAGCCGGTAATTGTATCTTGTAGAGCGCTTCCCATGTT 120  
Db 19336 ATGGCCCAACAGCTGGTAATTGTGTATCTAGAGCGCTTCCCATGTT 19277  
Qy 121 GCTCAGGCTGGCTCTGAACCTCAAACTCAGGTGATCGGCCCTGGCCCTCCAAAGT 180  
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/map="18g12"			
/clone="RP11-850H3"			
misc_feature	1. .33581		
/note="assembly_fragment"			
misc_feature	33682. .58093		
/note="assembly_fragment"			
misc_feature	58194. .77625		
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Query	GTATGGCACGATCTGTCACTGTCAGTCAACCTCAGGCCTCCAGTAGCTGGATTACAGGC	Score 38.4%; Best Local Similarity 82.7%; Matches 196; Conservative 0; Mismatches 41; Indels 0; Gaps 0;	Length 187200;
Qy	1 GTATGGCACGATCTGTCACTGTCAGTCAACCTCAGGCCTCCAGTAGCTGGATTACAGGC	Length 187200;	
Db	169862 GCAGTGGCGTGTGATCTAGCTCACGCCAACCTCAGACTCCGGATAGCTGGATTACAGGC	Length 187200;	
Qy	61 ATGGCCACCAAGCCGGCTTAATTGTATCTTTAGTAGAGGCCGTTCCTCATGTT	Length 187200;	
Db	169922 ATGCCACACGCCGTGGTAATTGTGTGTTACTAGAGGCCGTTCCTCATGTT	Length 187200;	
Qy	121 GGTCAGGCTGGCTCGAACTTCAAACCTCAGGTATCCGCCGCTCGAACCTCAGGATCTCCAAAGT	Length 187200;	
Db	169982 GGTCAGGCTGGCTGTGAATCCCCAACCTCAGTGATCCACCCGCCGCTCGAACCTCAGGATCTCCAAAGT	Length 187200;	
Qy	181 GCTAGGATTACGGGTGAGCCACGGCAACCTTTCCTTAATC	Length 187200;	
Db	170042 GCTGGGATTAACGGGTGAGCCACACGGGGCTGAAAGCTGTAATTTTAAAC	Length 187200;	
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/map="18g12"			GI:18464243
/clone="RP11-850H3"			
misc_feature	1. .33581		
/note="assembly_fragment"			
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LOCUS	AC064841	DEFINITION Homo sapiens BAC clone CTD-2015A10	69229 bp DNA linear
ACCESSION	AC064841	VERSION 1	PRI 21-FEB-2002
KEYWORDS	1 (bases 1 to 69829)	AUTHORS Sulston, J.E. and Waterston, R.	REFERENCE
SOURCE	Homo sapiens (human)	TITLE Toward a complete human genome sequence	
ORGANISM	Bukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.	JOURNAL Genome Res.	
		YEAR 1998	
		MEDLINE 99063732	
		PUBMED 9847074	
		REFERENCE 2 (bases 1 to 69829)	

AUTHORS Abbott, S. and Cotton, M.  
 TITLE The sequence of Homo sapiens BAC clone CTD-2015A10  
 JOURNAL Unpublished (2001)  
 3 (bases 1 to 69829)

AUTHORS Waterston, R. H.  
 TITLE Direct Submission  
 JOURNAL Submitted (23-APR-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA  
 REFERENCE 4 (bases 1 to 69829)  
 Waterston, R. H.  
 Direct Submission  
 Submitted (01-FEB-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA  
 REFERENCE 5 (bases 1 to 69829)  
 Waterston, R.  
 Direct Submission  
 Submitted (21-FEB-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA  
 On Feb 1, 2002 this sequence version replaced gi:8151025.

COMMENT -----  
 Genome Center  
 Center: Washington University Genome Sequencing Center  
 Center code: WUGSC  
 Web site: <http://genome.wustl.edu/gsc>  
 Contact: [sapiens@watson.wustl.edu](mailto:sapiens@watson.wustl.edu)  
 ----- Summary Statistics  
 Center project name: H\_MS2015A10  
 -----.

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:  
 Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:  
 Clone CTD-2015A10 is from a release of the human BAC library CTD. The library contains cloned DNA from human sperm. See: Shizuya et al., Proc. Natl. Acad. Sci. USA 89:8794-7 (1992); U-J. Kim et al., Genomics 34:213-8 (1996). The clone is available from Research Genetics, Inc. (<http://www.regen.com>).  
 VECTOR: pBeloBAC11  
 Selection: chloramphenicol

NEIGHBORING SEQUENCE INFORMATION:  
 The clone sequenced to the left is RP11-12J20, 2000 bp overlap; the clone sequenced to the right is RP11-765C7, 2000 bp overlap. Actual start of this clone is at base position 9533 of RP11-12J20; actual end is at base position 26527 of RP11-765C7.

FEATURES

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		/clone_lib="CTD"

repeat\_region 2. .160



FEATURES

source	1.	1.178670	Location/Qualifiers
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	/mol_type="genomic DNA"		
	/db_xref="txon:3606"		
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ORIGIN			

Query Match 38.3%; Score 171; DB 2; Length 178670;  
Best Local Similarity 66.9%; Pred. No. 3..28..30;  
Matches 243; Conservative 0; Mismatches 120; Indels 0; Gaps 0;

QY 1 GAAATGGCAGATCTCGTCACTGCAACTCCAGCTTGTGTTATTGCTGGATTACAGGC 60  
DB 50841 GCAATGGCAGATCTGGCTCACTGTAATCTCGCTCTCTGAGTAGCTGGATTACAGGC 50782  
QY 61 ATGCCCAACCAGGCCGGTAATTGTATCTTTAGTAGAGAGGCCCTCCCTCCATTT 120  
DB 50781 ATGCCAACCAACACTGGTAATTGTATTTAGTAGAGAGGCCCTCCATTT 50722

QY 121 GCTAGGATTAACAGGGTGAACCTCAACCTCAAGGATACGCCACCGTCAGCTGGAACACCTTCTCATCTC 240  
DB 50721 GGCCAGGGCTGGCTGAATCTGCACTCCATGTTAGGATCTCCGCTCCAGGT 50662

QY 181 GCTAGGATTAACAGGGTGAACCTCAACCTCAAGGATACGCCACCGTCAGCTGGAACACCTTCTCATCTC 240  
DB 50661 GCTGGGATTAACAGGGATACGCCACCGTCAGCTGGAACACCTTCTCATCTC 50602

QY 241 AAGTGCTGAAATGCTTGAAGAAAAGATTATAAGGTAATTATAAGAAAC 300  
DB 50601 CAGTTAAATGCTGTGTTAGGGAGGCCCTTCTGGCCATCTATTAAATTGTCTTT 50542

QY 301 ACTCATTCTTCCCAAAGAGAGGAAAGATTATAAGGTAATTATAAGAAAC 360  
DB 50541 TCCCTTCATTCTGAACTGTTAGTCTGTTACAGAACTTATTCTTCTT 50482

NOTICE: This sequence was finished as follows unless otherwise noted:  
all regions were double stranded, sequenced with an alternate  
chemistry, or covered by high quality data (i.e., phred quality >=  
30); an attempt was made to resolve all sequencing problems, such  
as compressions and repeats; all regions were covered by sequence  
from more than one subclone; and the assembly was confirmed by  
restriction digest.

MAPPING INFORMATION:  
Mapping information for this clone was provided by Dr. John D.

McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:  
The RPCI-11 human BAC library was made from the blood of one male donor, as described by Oseegawa,K., Woon,P.Y., Zhao,B., Freygen,E., Tateno,M., Catanese,J.J. and de Jong,P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (<http://bacpac.med.buffalo.edu>)

VECTOR: pbace3.6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the right is RP11-480N9. Actual start of this clone is at base position 1 of RP11-462M9; actual end is at base position 176075 of RP11-462M9.

The sequence H\_NH0462M09 from base positions 164804 to 164876 and 165220 to 165258 are represented by sequences derived from PCR on BAC DNA.

FEATURES      Location/Qualifiers

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repeat_region	/rpt_family="AT_rich"
misc_feature	1116..1459 /note="similar to EST BF329553 (NID:911300301)"
misc_feature	2003..2101 /note="similar to EST AU119468 (NID:911000989)"
misc_feature	2003..2101 /note="similar to EST AX085613 (NID:913275620)"
misc_feature	2003..2111 /note="similar to EST BE569397 (NID:99813657)"
misc_feature	2906..2929 /note="similar to EST AU119468 (NID:911000989)"
misc_feature	2906..2929 /note="similar to EST AX085613 (NID:913275620)"
repeat_region	3010..3382 /rpt_family="Alu"
misc_feature	3521..3864 /note="similar to EST BF901906 (NID:912293365)"
misc_feature	3766..3864 /note="similar to EST AU119468 (NID:911000989)"
misc_feature	3766..3864 /note="similar to EST AX085613 (NID:913275620)"
misc_feature	3766..3864 /note="similar to EST BE569397 (NID:99813657)"
misc_feature	3792..3864 /note="similar to EST BF159650 (NID:911039755)"
repeat_region	3810..3864 /note="similar to EST AA589501 (NID:92402881) v148c05.81" 4727..5223 /rpt_family="L1"
repeat_region	5495..5607 /rpt_family="L2"
repeat_region	5608..5911 /rpt_family="Alu"
repeat_region	5912..5947 /rpt_family="L2"

Query Match      38.3%; Score 170.6; DB 9; Length 176075;  
Best Local Similarity 69.8%; Pred. No. 4e-30;  
Matches 259; Conservative 0; Mismatches 109; Indels 3; Gaps 2;

QY      23 CTCGAACCTCAGCTCCCAAGTAGCTGGATTACAGGATCGCCACCAAGCTTAA  
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QY      83 TTGTGATCTTGTAGTAGACGGCGTTCCTCCATGTTGTCAGCTGTCTCCAGCTGTTCTCCAGCTGTTCTCCAGCTGTTCTCCAGCTGTTCTCCAGCTCC 91787  
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REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.
AUTHORS	Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C., Alisbrookes, S.L., Amararatne, H.C., Are, J.R., Ayelle, M., Banks, T., Barbaria, J., Benton, J., Blimkie, K., Blankenbogen, K., Bonnin, D., Bouch, J., Bowie, S., Brieva, M., Brown, E., Bryant, N.P., Buiay, C., Burch, P., Burkett, C., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chavez, D., Chen, G., Chen, R., Chen, Z., Chiu, D., Chowdhury, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Datheone, S.R., David, R., Hamilton, K., Han, J., Harris, C., Harris K., Hart, M., Havlik, P., Hawes, A., Hernandez, J., Hernandes, O., Hodson, A., Hogues, M., Holloway, C., Hollins, B., Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Ioshikhes, I., Jackson, L.E., Jacobson, B., Jia, Y., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lee, E., Lewis, L.C., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, W., Louise, H., Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Maheshwari, M., Maqua, P., Marondel, J., Martin, R., Martindale, A., Miner, Z., Mitchell, T., Matzkin, E., McLeod, M.P., Meadow, E., Massey, E., Mohabbat, K., Montgomery, K.T., Morgan, M., Morris, S., Moser, M., Neal, D., Nelson, D., Newton, J., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokonkwo, S., Ogpin, M., Okwonou, G., Oregunye, N., Oviedo, R., Pace, A., Payron, B., Peery, J., Perez, L., Peters, J., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Rives, M., Rotas, A., Rotubokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shim, C., Shnoohari, N., Sisson, I., Sodergran, B., Sonaike, T., Sparks, R., Stanley, R., Steffen, D., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tametisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, J., Usmani, K., Vasquez, L., Vera, V., Verduco, D., Villalon, D., Vinson, R., Waldron, L.M., Wang, Q., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Wheeler, D., Williams, G., Williamson, G., Wilecyk, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Kucherlapati, R., Weinstock, G., and Gibbs, R.	
TITLE	Unpublished	
JOURNAL		
REFERENCE	2 (bases 1 to 163515)	
AUTHORS	Worley, K.C.	
TITLE	Direct Submission	
JOURNAL		
REFERENCE	Submitted (27-APR-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA	
AUTHORS	Worley, K.C.	
TITLE	Submitted (18-JUN-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA	
JOURNAL		
REFERENCE	4 (bases 1 to 163515)	
AUTHORS	Worley, K.C.	
TITLE	Direct Submission	
JOURNAL		
REFERENCE	Submitted (19-MAR-2004) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA	
COMMENT	On Mar 19, 2004 this sequence version replaced gi:32702245.	
REFERENCE	INFORMATION: <a href="http://www.hgsc.bcm.tmc.edu/">http://www.hgsc.bcm.tmc.edu/</a> or email gc-help@bcm.tmc.edu	
AUTHORS		
TITLE		
JOURNAL		
REFERENCE	CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of	

REFERENCE	Escotto, M., Fall, S.T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Gara, N., Gill, R., Gorrell, J.H., Guerra, W., Gunaratne, P., Hale, S., Hamilton, K., Han, J., Harris, C., Harris K., Hart, M., Havlik, P., Hawes, A., Hernandez, J., Hernandes, O., Hodson, A., Hogues, M., Holloway, C., Hollins, B., Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Ioshikhes, I., Jackson, L.E., Jacobson, B., Jia, Y., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lee, E., Lewis, L.C., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, W., Louise, H., Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Maheshwari, M., Maqua, P., Marondel, J., Martin, R., Martindale, A., Miner, Z., Mitchell, T., Matzkin, E., McLeod, M.P., Meadow, E., Massey, E., Mohabbat, K., Montgomery, K.T., Morgan, M., Morris, S., Moser, M., Neal, D., Nelson, D., Newton, J., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokonkwo, S., Ogpin, M., Okwonou, G., Oregunye, N., Oviedo, R., Pace, A., Payron, B., Peery, J., Perez, L., Peters, J., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Rives, M., Rotas, A., Rotubokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shim, C., Shnoohari, N., Sisson, I., Sodergran, B., Sonaike, T., Sparks, R., Stanley, R., Steffen, D., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tametisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, J., Usmani, K., Vasquez, L., Vera, V., Verduco, D., Villalon, D., Vinson, R., Waldron, L.M., Wang, Q., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Wheeler, D., Williams, G., Williamson, G., Wilecyk, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Kucherlapati, R., Weinstock, G., and Gibbs, R.	the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.
AUTHORS		Annotations of FEATURES:
TITLE		STSS are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.
JOURNAL		Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.
REFERENCE		Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.
AUTHORS		SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.
TITLE		QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of low quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: <a href="http://www.hgsc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html">http://www.hgsc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html</a> .
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- \* 57170 68317: gap of unknown length
- \* 57171 68317: contig of 11047 bp in length
- \* 68318 79880: contig of unknown length
- \* 68318 79881: contig of 11563 bp in length
- \* 79881 79981: gap of unknown length
- \* 79981 95382: contig of 15402 bp in length
- \* 95382 95482: gap of unknown length
- \* 95482 115764: contig of 20282 bp in length
- \* 115765 115864: gap of unknown length
- \* 115865 141197: contig of 25933 bp in length
- \* 141197 141897: gap of unknown length
- \* 141898 165593: contig of 23696 bp in length.

ORGIN

Query Match 38.1%; Score 170; DB: 2; Length 165593;

Best Local Similarity 80.0%; Pred. No. 5.5e-30;

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Qy 61 ATGCCACACACGCCGCTAAATTGTATTTAGTAGAGATGGGTTTACCCCTTT 120

Db 74335 ATGAGCCACATGCTGCTAAATTGTATTTAGTAGAGATGGGTTTACCCCTTT 74394

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Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

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  4: geneseqn2001as:*
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  6: geneseqn002as:*
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 10: geneseqn2003cs:*
 11: geneseqn2003ds:*
 12: geneseqn2004s:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the total score of the result being printed, and is derived by analysis of the total score distribution.

Result		Query		Match		Length		DB		ID		Description		
No.	No.	Score	%	Match	Length	DB	ID	DB	ID	DB	ID	DB	Description	
1	446	100.0	4282	4	AAL41998	Human	GA7	AAL41998	Human	GA7	AAL41998	Human	GA7	
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3	169.6	38.0	4388	4	AAL04959	Human	rep	AAL04959	Human	rep	AAL04959	Human	rep	
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c	7	166.8	37.4	344	4	AAK68705	Human	imm	AAK68705	Human	imm	AAK68705	Human	imm
c	8	166	37.2	26878	8	AAD56105	Human	CCN	AAD56105	Human	CCN	AAD56105	Human	CCN
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c	17	162.4	36.4	185371	6	ABT10718	Human	bre	ABT10718	Human	bre	ABT10718	Human	bre
c	18	162.2	36.4	3200	6	ABK47724	Genomic	Abk47724	Genomic	s	Abk47724	Genomic	s	
c	19	162.2	36.4	160361	12	ADL08116	Human	gen	ADL08116	Human	gen	ADL08116	Human	gen
c	20	161.2	36.1	4779	14	AAL61042	Human	pol	AAL61042	Human	pol	AAL61042	Human	pol
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AC	AAL41898;
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DT	03-MAY-2002 (first entry)
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DE	Human GA733-2 gene (encoding human epithe-
XX	Human; GA733-2 gene promoter; gene; epith-
KW	pan-carcinoma associated antigen; cancer;
KW	treatment evaluation; non-squamous epithe-
KW	transgenic animal; ds; gene therapy.
XX	
OS	Homo sapiens.
XX	



Human; reproductive system related antigen; reproductive system disorder;  
cancer; gene therapy; ds.

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PR	01-SEP-2000; 20000US-0229344P.	PR	17-NOV-2000; 20000US-02449245P.
PR	01-SEP-2000; 20000US-0219345P.	PR	17-NOV-2000; 20000US-02449264P.
PR	05-SEP-2000; 20000US-0229509P.	PR	17-NOV-2000; 20000US-02449265P.
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PR	08-SEP-2000; 20000US-0231413P.	PR	05-DEC-2000; 20000US-0256719P.
PR	06-SEP-2000; 20000US-0230437P.	PR	06-DEC-2000; 20000US-0251779P.
PR	08-SEP-2000; 20000US-0229343P.	PR	08-DEC-2000; 20000US-0251856P.
PR	08-SEP-2000; 20000US-0231422P.	PR	08-DEC-2000; 20000US-0251868P.
PR	12-SEP-2000; 20000US-021968P.	PR	08-DEC-2000; 20000US-0251989P.
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PR	14-SEP-2000; 20000US-0233064P.	PR	14-SEP-2000; 20000US-02344988P.
PR	14-SEP-2000; 20000US-0233065P.	PR	14-SEP-2000; 20000US-02344988P.
PR	21-SEP-2000; 20000US-0234423P.	PR	21-SEP-2000; 20000US-0234423P.

PR 05-JAN-2001; 2001US-0259678P.  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 PR  
 XX Rosen CA, Barash SC, Ruben SM;  
 PI  
 XX Disclosure; SEQ ID NO 7647; 1297pp + Sequence Listing; English.  
 DR WPI; 2001-465570/50.  
 XX Isolated nucleic acid molecule encoding a reproductive system antigen is  
 PT used in preventing, treating or ameliorating a medical condition.  
 XX  
 Disclosure; SEQ ID NO 7647; 1297pp + Sequence Listing; English.  
 PR  
 XX The present invention provides the protein and coding sequences of a  
 CC number of human reproductive system related antigens. These can be used  
 CC in the prevention and treatment of reproductive system disorders,  
 CC including cancer. The present sequence is a genomic sequence encoding a  
 protein of the invention  
 XX Sequence 4388 BP; 870 A; 1238 C; 1205 G; 1075 T; 0 U; 0 Other;  
 SQ Query Match 38.0%; Score 169.6; DB 4; Length 4388;  
 Best Local Similarity 86.6%; Pred. No. 1.4e-28;  
 Matches 187; Conservative 0; Mismatches 29; Indels 0; Gaps 0;  
 Qy 1 GAAATGGCACGATCTGTCACTTCAGCTCAACCTCAGCCTCCCAAGTAGCTGGATTACAGGC 60  
 Db 1079 GCAATGGCACGATCTGTCACTTCAGCTCAACCTCAGCCTCCCAAGTAGCTGGATTACAGGC 1138  
 Qy 61 ATGGCGCACCAAGGCCGTAATTCTGTATCTTGTATAGAGAGGGCTTCGCTCCATGTT 120  
 Db 1139 GGCGCACCAACRGTCAGTGGCTGAATTCTGTATTTGTATTCTGTATAGAGACGGAGTTTACCATTT 1198  
 Qy 121 GGTCAGGGCTGGCTGAACCTCAAACTCAGGTATCCGGCTCCGAAGT 180  
 Db 1199 GGCCAGGTCTGGCTGAACCTCCTGACCTCAAGTGTATCCGGCTCCGAAGT 1258  
 Qy 181 GCTAGGATTACAGGGTGACGCCAGGGTCAGGCT 216  
 Db 1259 GCTGGAATTACAGGGTGACGCCAGGGTCAGGCT 1294

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RESULT<sup>4</sup>  
 ABL97853 ID ABL97853 standard; DNA; 4388 BP.  
 XX  
 AC ABL97853;  
 DT 21-JUN-2002 (first entry)  
 XX Human testicular antigen encoding DNA fragment SEQ ID NO: 2505.  
 DE Human testicular antigen encoding DNA fragment SEQ ID NO: 2505.  
 XX Human; testicular antigen; testes; cancer; metastasis; immune disorder;  
 KW reproductive system disorder; urinary system disorder; gene therapy;  
 KW cardiovascular disorder; respiratory disorder; neurological disorder;  
 KW gastrointestinal disease; infection; cytostatic; gene; ds.  
 XX Homo sapiens.  
 XX WO200115517-A2.  
 PD 02-AUG-2001.  
 XX 17-JAN-2001; 2001WO-US001329.  
 XX  
 PR 31-JAN-2000; 2000US-019965P.  
 PR 04-FEB-2000; 2000US-0180628P.  
 PR 24-FEB-2000; 2000US-0184664P.  
 PR 02-MAR-2000; 2000US-0186350P.  
 PR 16-MAR-2000; 2000US-0199874P.  
 PR 17-MAR-2000; 2000US-0190076P.  
 PR 18-APR-2000; 2000US-0198123P.  
 PR 19-MAY-2000; 2000US-0205515P.  
 PR 07-JUN-2000; 2000US-0209467P.  
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 PR 06-SEP-2000; 2000US-0230438P.  
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 PR 08-SEP-2000; 2000US-0231243P.  
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 PR 08-SEP-2000; 2000US-0231413P.  
 PR 08-SEP-2000; 2000US-0232080P.  
 PR 08-SEP-2000; 2000US-0232081P.  
 PR 12-SEP-2000; 2000US-0232398P.  
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 PR 29-SEP-2000; 2000US-02363169P.  
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 PR 20-OCT-2000; 2000US-0241221P.

PR 20-OCT-2000; 2000US-0241785P.  
 PR 20-OCT-2000; 2000US-0241786P.  
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 PR 17-NOV-2000; 2000US-0249215P.  
 PR 17-NOV-2000; 2000US-0249216P.  
 PR 17-NOV-2000; 2000US-0249217P.  
 PR 17-NOV-2000; 2000US-0249218P.  
 PR 17-NOV-2000; 2000US-0249244P.  
 PR 17-NOV-2000; 2000US-0249245P.  
 PR 17-NOV-2000; 2000US-0249264P.  
 PR 17-NOV-2000; 2000US-0249265P.  
 PR 17-NOV-2000; 2000US-0249279P.  
 PR 17-NOV-2000; 2000US-0249300P.  
 PR 01-DEC-2000; 2000US-0250160P.  
 PR 01-DEC-2000; 2000US-0250319P.  
 PR 05-DEC-2000; 2000US-0251030P.  
 PR 05-DEC-2000; 2000US-0251988P.  
 PR 06-DEC-2000; 2000US-0251479P.  
 PR 08-DEC-2000; 2000US-0251856P.  
 PR 08-DEC-2000; 2000US-0251869P.  
 PR 08-DEC-2000; 2000US-0251989P.  
 PR 08-DEC-2000; 2000US-0254490P.  
 PR 11-DEC-2000; 2000US-0254497P.  
 PR 05-JAN-2001; 2001US-0259678P.  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 PI Rosen CA, Barash SC, Ruben SM;  
 XX DR WPI; 2001-483232/52.  
 PT Nucleic acids encoding 973 human testicular antigen polypeptides, useful  
 PT for preventing, diagnosing and/or treating testicular cancer.  
 PS Disclosure; SEQ ID NO 2505; 766pp; English.  
 CC The present invention provides the protein and coding sequences of 973  
 CC human testicular antigens, and fragments of their genomic sequences. The  
 CC sequences can be used in the treatment of cardiovascular, urinary system,  
 CC reproductive system, immune, respiratory, neurological and  
 CC gastrointestinal disorders, infections, and particularly cancer,  
 CC especially testicular cancers. The present sequence is a DNA encoding a  
 CC protein fragment of the invention  
 XX Sequence 438B BP; 870 A; 1238 C; 1205 G; 1075 T; 0 U; 0 Other;  
 SQ Query Match 38.0%; Score 169.6%; DB 4; Length 4388;  
 Best Local Similarity 86.6%; Pred. No. 1.4e-28;  
 Matches 187; Conservative 0; Mismatches 29; Indels 0; Gaps 0;  
 Qy 1 GTATGGCACGATCTGCTACTCAACCTCAGGCTCCCGTAGCTGGGATACAGGG 60  
 Db 1079 GCAATGGCACGATCTGCTGGTCAAACCTCCGCTCCGGAGTAGCTGGGATACAGGG 1138  
 Qy 61 ATGGGCCAACACGGGGTAATTGTATCTTTAGTAGAGAAGGGGGTTCCTCGATGTT 1200  
 Db 1139 GGCGCCAACACGGGGTAATTGTATTTAGTAGAGAAGGGAGTTCAACCATGTT 1198  
 Qy 121 GGTCAGGGCTGGTCTGAACCTCAACCTCAGGTAATTGTATCTGGCTCCGCTCCAAAGT 1800  
 Db 1199 GGCGAGGCTGGTCTGAACCTCAGCTGACCTCAAGTATCCGGGCTCGGCTCCAAAGT 1258  
 Qy 181 GCTAGGATTACGGCGTGACGCCACGGCTCAAGCT 216  
 Db 1259 GCTGGAATTACGGTTGAGTCATTCGCCCCCT 1294

RESULT 5  
 ADM01919 ID ADM01919 Standard; cDNA; 3252 BP.  
 XX  
 AC ADM01919;  
 XX DT 20-MAY-2004 (first entry)  
 DE Human cDNA of the invention SEQ ID NO:604.  
 XX  
 KW ss; gene; human; gene therapy; diagnostic marker; pharmaceutical.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EP1347046-A1.  
 XX  
 PD 24-SEP-2003.  
 XX  
 PP 12-APR-2002; 2002EP-00008400.  
 XX  
 PR 22-MAR-2002; 2002JP-00137785.  
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
 XX  
 PI Issai T, Sugiyama T, Otsuki H, Ishii S; Wakamatsu A, Nagai K, Irie R, Tamechika I;  
 PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagahari K, Masuho Y;  
 PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;  
 DR WPI; 2003-723558/69.  
 DR P-PSDB; ADM013362.  
 XX  
 PT New polynucleotides and polypeptides are useful in gene therapy, for  
 PT developing a diagnostic marker or medicines for regulating their  
 PT expression and activity, or as a target of gene therapy.  
 XX  
 PS Claim 1; SEQ ID NO 604; 305pp; English.  
 XX  
 CC The invention relates to a novel human polynucleotide and the encoded  
 CC polypeptide. A polynucleotide of the invention may have a use in gene  
 CC therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful  
 CC as a primer for synthesizing the polynucleotide or as a probe for  
 CC detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are  
 CC useful in gene therapy, for developing a diagnostic marker or medicines  
 CC for regulating their expression and activity, or as a target of gene  
 CC therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides  
 CC are useful as pharmaceutical agents. The present sequence represents a  
 CC cDNA sequence of the invention.  
 XX

SQ Sequence 3252 BP; 817 A; 802 C; 835 G; 798 T; 0 U; 0 Other;  
 Best Local Similarity 37.9%; Score 169.2; DB 11; Length 3252;  
 Matches 195; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 1 GTAAATGCCAGATCTGGTCACTGCAACCTCAGGTGGATTACAGGC 60  
 Db 2742 GCAGNGGCAATCTCGACGTCACGTTCCAGCTTCAAGGTTACAGGC 2801

QY 61 ATGCGCACCAACGCCGGCTTAATTTGTATCTTTAGTAGAGACGGCGTCCCTCATGTT 120  
 Db 2802 ACGTACCAACCAACGCCCTGGCTTAATTTGTTTATAGTAGAGGGGTTACAGGT 2861

QY 121 CGTCAGGCTGGTCTCGAACCTCAGGTGATCCGGCCGCTCCGCCTCCAAACT 180  
 Db 2862 GGCCAGGTGGTCTCAAACTCTGACCTCTGATCAGTCAGCTCCAAACT 2921

QY 181 GCTAGGATTACAGGGGTGAGCCACGGGCTCAGCTGGAAACACCTTCTTACATC 238

Db 2922 ACTGGGATTACAGGGTGAGCCACTGGCCAACTGTGAGGACCTTAAATACATT 2979

**RESULT 6**  
 ADN06353\_3/C  
 Continuation (4 of 4) of ADN06353 from base 300001 (Human FLAP Genomic DNA SEQ ID NO:1.  
 WP Sequence split into 4 fragments Locus ADN06353 Accession Adn06353  
 WP Fragment Name Begin End  
 WP ADN06353\_0 1 110000  
 WP ADN06353\_1 100001 210000  
 WP ADN06353\_2 200001 310000  
 WP ADN06353\_3 300001 398800

Query Match 37.9%; Score 169.2; DB 12; Length 98800;  
 Best Local Similarity 85.1%; Pred. No. 3.3e-28;  
 Matches 189; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 23 CTGGCAACTCTAGCCTCCCGAGTAGTGGGATTACAGGATGCGCACACGCCGGCTAA 82  
 Db 81352 CTCCCTGCTCTGCTCCGGTAGTGGGATTACAGGATGCCACACGCTGGCTGA 81293

QY 83 TTTTGTATCTTTAGTAGAGACGGGTTCCTCCATGTTGGTACGGCTGTCGAACCTTC 142  
 Db 81292 TTTCCTATTTTTAGTAGAGATGGTTCTCCATGTTGGTACGGCTGTCGAACCTC 81233

QY 143 AAACCTCACTGATGCTGGCTCCAAAGTGTAGGATTACGGGTGACGCC 202  
 Db 81232 TGACCTCACTGATGCTGGCTCCAAAGTGTGGGATTACGGGTGACGCC 81173

QY 203 ACCGGCTCAGCTGGAAACACCTTCTTACATCTTCACT 244  
 Db 81172 ACCACGCCAGCCAACTCCATTCTCAAAGCTTTAAT 81131.

**RESULT 7**  
 AAK68705/C  
 ID AAK68705 standard; DNA; 344 BP.  
 XX  
 XX 06-NOV-2001 (first entry)  
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23517.  
 KW Human; immune; haematopoietic; immune/haemopoietic antigen; cancer;  
 KW cyrostatic; gene therapy; vaccine; metastasis; ds.  
 OS Homo sapiens.  
 XX  
 PN WO00157182-A2.  
 XX  
 PD 09-AUG-2001.

SQ Sequence 3252 BP; 817 A; 802 C; 835 G; 798 T; 0 U; 0 Other;  
 Best Local Similarity 37.9%; Score 169.2; DB 11; Length 3252;  
 Matches 195; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 1 GTAAATGCCAGATCTGGTCACTGCAACCTCAGGTGGATTACAGGC 60  
 Db 2742 GCAGNGGCAATCTCGACGTCACGTTCCAGCTTCAAGGTTACAGGC 2801

QY 61 ATGCGCACCAACGCCGGCTTAATTTGTATCTTTAGTAGAGACGGCGTCCCTCATGTT 120  
 Db 2802 ACGTACCAACCAACGCCCTGGCTTAATTTGTTTATAGTAGAGGGGTTACAGGT 2861

QY 121 CGTCAGGCTGGTCTCGAACCTCAGGTGATCCGGCCGCTCCGCCTCCAAACT 180  
 Db 2862 GGCCAGGTGGTCTCAAACTCTGACCTCTGATCAGTCAGCTCCAAACT 2921

QY 181 GCTAGGATTACAGGGGTGAGCCACGGGCTCAGCTGGAAACACCTTCTTACATC 238

Db 2922 ACTGGGATTACAGGGTGAGCCACTGGCCAACTGTGAGGACCTTAAATACATT 2979

PR 17-JAN-2001; 2001WO-US001354.  
 XX  
 PR 31-JAN-2000; 2000US-0179065P.  
 PR 04-FEB-2000; 2000US-0180628P.  
 PR 24-FEB-2000; 2000US-0184664P.  
 PR 02-MAR-2000; 2000US-0186350P.  
 PR 16-MAR-2000; 2000US-0189748P.  
 PR 17-MAR-2000; 2000US-0190078P.  
 PR 18-APR-2000; 2000US-0191228P.  
 PR 19-MAY-2000; 2000US-0205515P.  
 PR 07-JUN-2000; 2000US-0209467P.  
 PR 28-JUN-2000; 2000US-0214888P.  
 PR 30-JUN-2000; 2000US-0215135P.  
 PR 07-JUL-2000; 2000US-0216641P.  
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 PR 11-JUL-2000; 2000US-0217929P.  
 PR 14-JUL-2000; 2000US-0218200P.  
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 PR 07-JUL-2000; 2000US-0220964P.  
 PR 14-AUG-2000; 2000US-0224519P.  
 PR 14-AUG-2000; 2000US-0225213P.  
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 PR 14-AUG-2000; 2000US-0225267P.  
 PR 14-AUG-2000; 2000US-0225268P.  
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 PR 22-AUG-2000; 2000US-0227152P.  
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 PR 01-SEP-2000; 2000US-0229287P.  
 PR 01-SEP-2000; 2000US-0229343P.  
 PR 01-SEP-2000; 2000US-0229344P.  
 PR 01-SEP-2000; 2000US-0229345P.  
 PR 05-SEP-2000; 2000US-0229509P.  
 PR 06-SEP-2000; 2000US-0229513P.  
 PR 06-SEP-2000; 2000US-0230437P.  
 PR 06-SEP-2000; 2000US-0230439P.  
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 PR 14-SEP-2000; 2000US-0232401P.  
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 PR 21-SEP-2000; 2000US-0234223P.  
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PR 29-SEP-2000; 2000US-0236370P.  
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 PR 02-OCT-2000; 2000US-0237038P.  
 PR 02-OCT-2000; 2000US-0237039P.  
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 PR 13-OCT-2000; 2000US-0239937P.  
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 PR 17-NOV-2000; 2000US-0249217P.  
 PR 17-NOV-2000; 2000US-0249218P.  
 PR 17-NOV-2000; 2000US-0249244P.  
 PR 17-NOV-2000; 2000US-0249245P.  
 PR 17-NOV-2000; 2000US-0249264P.  
 PR 17-NOV-2000; 2000US-0249265P.  
 PR 17-NOV-2000; 2000US-0249297P.  
 PR 17-NOV-2000; 2000US-0249399P.  
 PR 06-DEC-2000; 2000US-0251479P.  
 PR 06-DEC-2000; 2000US-0251490P.  
 PR 01-DEC-2000; 2000US-0250164P.  
 PR 01-DEC-2000; 2000US-0250166P.  
 PR 05-DEC-2000; 2000US-0251030P.  
 PR 05-DEC-2000; 2000US-0251030P.  
 PR 05-DEC-2000; 2000US-0251989P.  
 PR 08-DEC-2000; 2000US-0256719P.  
 PR 08-DEC-2000; 2000US-0256719P.  
 PR 11-DEC-2000; 2000US-0254097P.  
 PR 05-JAN-2001; 2001US-0259678P.  
 XX (HUMA) HUMAN GENOME SCI INC.  
 XX PI Rosen CA, Barash SC, Ruben SM;  
 XX DR WPI; 2001-483426/52.  
 XX PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides,

PT useful for preventing, diagnosing and/or treating cancers and metastasis.  
 XX Disclosure; SEQ ID NO 23517; 3071PP + Sequence Listing; English.  
 PS XX  
 PS AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91321. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patient's own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK64703 to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAM82169 represent sequences used in the exemplification of the present invention.  
 XX SQ Sequence 344 BP; 91 A; 93 C; 90 G; 70 T; 0 U; 0 Other;  
 XX Query Match 37.4%; Score 166.8; DB 4; Length 344;  
 XX Best Local Similarity 85.3%; Pred. No. 34e-28;  
 XX Matches 186; Conservative 0; Mismatches 32; Indels 0; Gaps 0;  
 Qy 23 CTGCAACCTAGCCTCCAGTAGTGGATTAGGATGCGCATGCCGGCTAA 82  
 Db 253 CTCTGGCCCTAGCCTCCGGAGTAGCTGGATTAGGATGCCATGCCAGCTAA 194  
 Qy 83 TTTCSTATTTTACTAGAGACGGGTCTCCATGTTGTTGTTGCTGAACTTC 142  
 Db 193 TTTCATTTAGTTAGATGGTTCTCCATGTTGTTGCTGAACTTC 134  
 Qy 143 AACCTCAGGTGATCGCCGCCGCGCTCCAAAGTCTAGGATTACAGGGCTGAGCC 202  
 Db 133 AGACCTCAGGTGATCGCCGCCGCTAGTCCTCCAAAGTCTGGATTACAGGGCTGAGCC 74  
 Qy 203 ACCGGCTAGCCGGACACCTTTCTACATCTTC 240  
 Db 73 ACTGGCCGGCTGATATAAACTTTAAAACGGCTC 36  
 RESULT B  
 AAD56105/c  
 ID AAD56105 standard; DNA; 26874 BP.  
 XX AC AAD56105;  
 XX DT 07-AUG-2003 (first entry)  
 XX Human CCND3 carcinoma associated (CA) gene.  
 XX DE WO2003035837-A2.  
 XX KW Carcinoma; gene therapy; carcinoma associated gene; CA; CCND3; human; Homo sapiens.  
 XX OS PR 22-OCT-2002; 2002WO-US33835.  
 XX PN PR 23-OCT-2001; 2001US-0004113.  
 XX PA (SAGR-) SAGRES DISCOVERY.  
 XX DR Engelhard EK, Morris DW;  
 XX PR WPI; 2003-421412/39.  
 XX PT

binds to the protein, and a biochip comprising CA nucleic acid or fragments thereof. The sequences of the invention were identified using oncogenic retroviruses, which insert into the genome of the host organism at random. Many of these do not carry transduced host oncogenes or pathognomic trans-acting viral genes, meaning that cancer incidence is a direct consequence of the effects of proviral integration into host protooncogenes. The CA nucleic acid sequences can be used to diagnose carcinoma (especially breast cancer, prostate cancer, lymphoma or leukaemia) or a propensity to carcinoma by determination of the sequence of a CA gene, or by determination of CA gene expression in particular tissues. CA nucleic acids, proteins and antibodies are also useful as therapeutic agents and in screening and evaluating drug candidates. The present sequence represents a specifically claimed human CA nucleic acid sequence of the invention. Note: The complete sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [ftp://wipo.int/pub/published\\_pct\\_sequences](ftp://wipo.int/pub/published_pct_sequences).

Sequence 26874 BP; 6621 A; 6602 C; 6751 G; 6880 T; 0 U; 20 Other;

query Match	37.2%	Score 166;	DB 9;	Length 26874;
best Local Similarity	81.1%	Pred. No.	1. 3e-27;	
matches 193;	Conservative	0;	Mismatches	45;
			Indels	0;
			Gaps	0;

1 GTAAATGGCAGATCTGTCTACTGAAACCTCAGCCCTCCCAAGTAGCTGGATTACAGGC  
 22835 GCATGGATGTCACTCACTGAACTCAGCAACCTCAGCCCTCCCAAGTAGCTGGATTACAGGC 22776

61 ATGCCCAACCACGCCGCTAATTGTATCTTTAGTAGAGCGGCCATTCTCCATGTT 120  
 22775 ACCTTACACCACCCCTGCTTAATTTTTATTAGTAGAGCAGGGTTTCACCATGTT 22716

121 GGTCAGGCTGGTCTGAACCTCAAACTCAGGTGATGCCCTCGCCCTCCAAAGT 180  
 22715 GGCCAGGCTGGTCTCAAACTCTGACCTCACGTGATCCACCTCCCTAGCCTCCAAAGT 22656

181 GCTAGGATTACAGGGTGAGCCACCGGCTCAACCTGGAACACCTTCTTACATCT 238  
 22655 ACTGGGATTACAAGGTAGCCACTGGCCCAAATGGAAGCAGCTTAATACATT 22598

WUFL 10

7/22/06/c ADB72206 Standard; DNA; 26874 BP.

ADB72206;

04-DEC-2003 (first entry)

Human CCND3 gene.

Homo sapiens.

WO2003008583-A2.

30-JAN-2003.

26-DEC-2001; 2001WO-US051291.

02-MAR-2001; 2001US-0079886.  
 23-OCT-2001; 2001US-0000413.  
 08-NOV-2001; 2001US-0005282.  
 30-NOV-2001; 2001US-0097722.  
 20-DEC-2001; 2001US-0003450.

(SAGR-) SAGRES DISCOVERY.

Morris DW, Englehardt EK;

WPI; 2003-239337/23.

XX New recombinant nucleic acid, useful for treating carcinomas, lymphomas, cancers, neoplasm, adenocarcinoma, or sarcomas.

PT PT

XX XX

PS PS

Claim 1; SEQ ID NO 34; 2304pp; English.

CC The invention relates to a novel recombinant nucleic acid comprising a nucleotide sequence selected from any of the 650 sequences fully defined in the specification. A polynucleotide of the invention has cytosinic activity, and may have a use in gene therapy, or in a vaccine. The recombinant nucleic acids and polypeptides are useful for treating carcinomas, e.g. lymphomas, cancers, neoplasm, adenocarcinoma, and sarcomas. The present sequence represents a human gene of the invention.

XX Sequence 26874 BP; 6621 A; 6602 C; 6751 G; 6880 T; 0 U; 20 Other;

Query Match 37.2%; Score 166; DB 10; Length 26874;

Best Local Similarity 81.1%; Pred. No. 1.3e-27;

Matches 193; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 1 GAAATCGCACGATCTGTGTCACAGCAACCTCAGGGTCCCAGTAGCTGGATTACAGGC 60

Db 22835 GCAGTGCGATGATCTAGCTCACTCGACTCAACCTCAGCTCTGAGTAGCTGGATTACAGGC 22776

QY 61 ATGGGCCACACAGCCGGCTAAATTGGTATCTTTAGTAGAGACGGGTCTCCATGTT 120

Db 22775 AGTGTACACCAGCCGGCTGTAAATTGGTATCTTTAGTAGAGACGGGTCTCCATGTT 22716

QY 121 GGTCAGGTGGTCTCAACCTCAACCTCAGGTGATCAGCCGCTCGGCCTCCAAGT 180

Db 22715 GGCCAGGTGGTCTCAACCTCTGACCTCAACCTCTGACCTCAGCTGATCAGCTCCCTCAAAGT 22656

QY 181 CCTAGGATTAGGGCTGAGGCCACGGCTAGCCGGCTAGCCCTGGGACACCTTCTTACATCT 238

Db 22655 ACTGGAATTAAAGCTGAGCCACTGAGCTAAACTGAGAACGTTAAATAACATT 22598

RESULT 11  
ID AAK78202/c  
XX AAK78202 standard; DNA; 22651 BP.

AC AC

XX XX

DT 07-NOV-2001 (first entry)

XX Human immune/haematopoietic antigen genomic sequence SEQ ID NO:33014.

DE DE

KW KW

KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;

KW cytosstatic; gene therapy; vaccine; metastasis; ds.

XX Homo sapiens.

XX WO2001157182-A2.

XX XX

PD 09-AUG-2001.

PF 17-JAN-2001; 2001WO-US001354.

XX XX

PR 31-JAN-2000; 2000US-0179055P.

PR 04-FEB-2000; 2000US-0180628P.

PR 24-FEB-2000; 2000US-0184664P.

PR 02-MAR-2000; 2000US-018630P.

PR 16-MAR-2000; 2000US-0189874P.

PR 17-MAR-2000; 2000US-0190076P.

PR 18-APR-2000; 2000US-0198123P.

PR 19-MAY-2000; 2000US-0205151P.

PR 07-JUN-2000; 2000US-0209467P.

PR 28-JUN-2000; 2000US-0211886P.

PR 30-JUN-2000; 2000US-0215135P.

PR 07-JUL-2000; 2000US-0216647P.

PR 11-JUL-2000; 2000US-021487P.

PR 11-JUL-2000; 2000US-0217496P.

PR 01-NOV-2000; 2000US-0244617P.

PR 14-JUL-2000; 2000US-0218290P.

PR 26-JUL-2000; 2000US-0220963P.

PR 14-AUG-2000; 2000US-0224518P.

PR 14-AUG-2000; 2000US-0225213P.

PR 14-AUG-2000; 2000US-0225214P.

PR 14-AUG-2000; 2000US-0225266P.

PR 14-AUG-2000; 2000US-0225267P.

PR 14-AUG-2000; 2000US-0225270P.

PR 14-AUG-2000; 2000US-0225447P.

PR 14-AUG-2000; 2000US-0225757P.

PR 14-AUG-2000; 2000US-0225758P.

PR 14-AUG-2000; 2000US-0225759P.

PR 18-AUG-2000; 2000US-0226681P.

PR 22-AUG-2000; 2000US-0226868P.

PR 22-AUG-2000; 2000US-0227182P.

PR 30-AUG-2000; 2000US-0227009P.

PR 01-SEP-2000; 2000US-0229287P.

PR 2000US-0229343P.

PR 01-SEP-2000; 2000US-0229344P.

PR 01-SEP-2000; 2000US-0229345P.

PR 05-SEP-2000; 2000US-0229513P.

PR 06-SEP-2000; 2000US-0220437P.

PR 08-SEP-2000; 2000US-0220438P.

PR 08-SEP-2000; 2000US-0221242P.

PR 08-SEP-2000; 2000US-0221243P.

PR 08-SEP-2000; 2000US-0221244P.

PR 08-SEP-2000; 2000US-0221414P.

PR 08-SEP-2000; 2000US-02212080P.

PR 08-SEP-2000; 2000US-02212081P.

PR 12-SEP-2000; 2000US-0221968P.

PR 14-SEP-2000; 2000US-0221397P.

PR 14-SEP-2000; 2000US-0222398P.

PR 14-SEP-2000; 2000US-0222401P.

PR 14-SEP-2000; 2000US-0233063P.

PR 14-SEP-2000; 2000US-0233064P.

PR 14-SEP-2000; 2000US-0233065P.

PR 21-SEP-2000; 2000US-0234223P.

PR 21-SEP-2000; 2000US-0234274P.

PR 25-SEP-2000; 2000US-0234997P.

PR 25-SEP-2000; 2000US-0234998P.

PR 26-SEP-2000; 2000US-025484P.

PR 27-SEP-2000; 2000US-0255834P.

PR 27-SEP-2000; 2000US-0255836P.

PR 29-SEP-2000; 2000US-0236327P.

PR 29-SEP-2000; 2000US-0236367P.

PR 13-OCT-2000; 2000US-0237040P.

PR 13-OCT-2000; 2000US-0239935P.

PR 13-OCT-2000; 2000US-0239937P.

PR 02-OCT-2000; 2000US-0237038P.

PR 02-OCT-2000; 2000US-0237039P.

PR 02-OCT-2000; 2000US-0237040P.

PR 20-OCT-2000; 2000US-0241221P.

PR 20-OCT-2000; 2000US-0241785P.

PR 20-OCT-2000; 2000US-0241786P.

PR 20-OCT-2000; 2000US-0241808P.

PR 20-OCT-2000; 2000US-0241809P.

PR 20-OCT-2000; 2000US-0241826P.

PR 08-NOV-2000; 2000US-0246474P.  
 PR 08-NOV-2000; 2000US-0246475P.  
 PR 08-NOV-2000; 2000US-0246476P.  
 PR 08-NOV-2000; 2000US-0246477P.  
 PR 08-NOV-2000; 2000US-0246478P.  
 PR 08-NOV-2000; 2000US-0246523P.  
 PR 08-NOV-2000; 2000US-0246524P.  
 PR 08-NOV-2000; 2000US-0246525P.  
 PR 08-NOV-2000; 2000US-0246526P.  
 PR 08-NOV-2000; 2000US-0246527P.  
 PR 08-NOV-2000; 2000US-0246528P.  
 PR 08-NOV-2000; 2000US-0246531P.  
 PR 08-NOV-2000; 2000US-0246532P.  
 PR 08-NOV-2000; 2000US-0246533P.  
 PR 08-NOV-2000; 2000US-0246534P.  
 PR 08-NOV-2000; 2000US-0246535P.  
 PR 08-NOV-2000; 2000US-0246536P.  
 PR 08-NOV-2000; 2000US-0246610P.  
 PR 08-NOV-2000; 2000US-0246611P.  
 PR 08-NOV-2000; 2000US-0246613P.  
 PR 17-NOV-2000; 2000US-0246207P.  
 PR 17-NOV-2000; 2000US-0246208P.  
 PR 17-NOV-2000; 2000US-0246209P.  
 PR 17-NOV-2000; 2000US-0246210P.  
 PR 17-NOV-2000; 2000US-0246211P.  
 PR 17-NOV-2000; 2000US-0246212P.  
 PR 17-NOV-2000; 2000US-0246213P.  
 PR 17-NOV-2000; 2000US-0246214P.  
 PR 17-NOV-2000; 2000US-0246215P.  
 PR 17-NOV-2000; 2000US-0246217P.  
 PR 17-NOV-2000; 2000US-0246217P.  
 PR 17-NOV-2000; 2000US-0246221P.  
 PR 17-NOV-2000; 2000US-0246224P.  
 PR 17-NOV-2000; 2000US-0246225P.  
 PR 17-NOV-2000; 2000US-0246226P.  
 PR 17-NOV-2000; 2000US-0246227P.  
 PR 17-NOV-2000; 2000US-0246229P.  
 PR 17-NOV-2000; 2000US-0246229P.  
 PR 01-DEC-2000; 2000US-0249245P.  
 PR 01-DEC-2000; 2000US-0249246P.  
 PR 01-DEC-2000; 2000US-0249247P.  
 PR 05-DEC-2000; 2000US-0249297P.  
 PR 05-DEC-2000; 2000US-0249297P.  
 PR 06-DEC-2000; 2000US-0249300P.  
 PR 08-DEC-2000; 2000US-0251479P.  
 PR 08-DEC-2000; 2000US-0251856P.  
 PR 08-DEC-2000; 2000US-0251868P.  
 PR 08-DEC-2000; 2000US-0251869P.  
 PR 08-DEC-2000; 2000US-0251989P.  
 PR 08-DEC-2000; 2000US-0251990P.  
 PR 11-DEC-2000; 2000US-0254079P.  
 PR 05-JAN-2001; 2001US-0259678P.  
 XX PA (HUMA-) HUMAN GENOME SCI INC.  
 XX PI Rosen CA, Barash SC, Ruben SM;  
 XX DR WPI; 2001-483426/5Z.  
 XX PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.  
 XX Disclosure; SEQ ID NO 33014; 307pp + Sequence Listing; English.  
 CC AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patient's own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/hematopoietic-related diseases, especially  
 CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703 to AAK7694 represent human immune/hematopoietic antigenic genomic sequences from the present invention. AAK54942 to AAK54950 and AAM82169 represent sequences used in the exemplification of the present invention  
 XX Sequence 22651 BP; 5939 A; 5107 C; 5360 G; 6245 T; 0 U; 0 Other;  
 Query Match 37.0%; Score 165.2%; DB 4; Length 22651;  
 Best Local Similarity 90.7%; Pred. No. 1.9e-27;  
 Matches 176; Conservative 0; Mismatches 18; Indels 0; Gaps 0;  
 Qy 23 CTCGAACTCAGCTCCCACTGGATACAGCATGGCGCACCGCCGGCTAA 82  
 Db 4434 CTCCTGCCCTAGCTCCCAAAGTAGCTGGATACAGCATGGCGCACCGCCGGCTAA 4375  
 Qy 83 TTGTGATCTTTAGTAGAGACCGGTCCATTGTTGCTGGTGTGAACTTC 142  
 Db 4374 TTGTGATTTTTAGTAGAGATGGGTTTCCTCTGGTGTGAACTTC 4315  
 Qy 143 AACCTCAGGTATCCGCCCTGGCTCCACAAAGTGCTAGATTACAGGGTGAGCC 202  
 Db 4314 CAACTCAGGTATCCGCCCTAGTCTCCAAAGTGCTGAATTACAGGGTGAGCC 4255  
 Qy 203 ACCGGCTCAGCT 216  
 Db 4254 ACCGACCCAGCT 4241  
 RESULT 12  
 ADE95968  
 ID ADE95968 standard; DNA; 96596 BP.  
 XX AC ADE95968;  
 XX DT 12-FEB-2004 (first entry)  
 XX DE Human NFATC1 gene genomic DNA sequence.  
 XX KW cancer diagnosis; cancer treatment; carcinoma; cytostatic; gene therapy;  
 XX lymphoma; breast cancer; prostate cancer; leukaemia; ds; human; NFATC1.  
 XX OS Homo sapiens.  
 XX PN WO2003039484-A2.  
 XX PD 15-MAY-2003.  
 XX PR 08-NOV-2002; 2001US-00052482.  
 XX WPI (SAGR-) SAGRES DISCOVERY.  
 XX PI Morris DW, Engelhardt EK;  
 XX PR 08-NOV-2001; 2001US-00052482.  
 XX WPI; 2003-441462/41.  
 XX PA (SAGR-) SAGRES DISCOVERY.  
 XX PT New carcinoma associated nucleic acids and proteins, useful for screening drug candidates, or for diagnosing and treating carcinomas, e.g.,  
 XX PT lymphoma, breast cancer, prostate cancer or leukemia.  
 XX PS Claim 1; SEQ ID NO 226; 793pp; English.  
 XX DR This invention relates to novel recombinant nucleic acids for use in diagnosis and treatment of cancer, especially carcinomas, as well as the use of compositions in screening methods. The compositions of the invention may have cytostatic activity whilst the disclosed sequences may be useful for gene therapy. The carcinoma associated nucleic acids and proteins are useful for diagnosing and treating carcinomas, for example lymphoma, breast cancer, prostate cancer or leukaemia, or for screening drug candidates or bioactive agents capable of binding to, or modulating the activity of, a carcinoma associated protein. The present sequence is the genomic DNA sequence of the human NFATC1 gene which is a carcinoma  
 CC

CC associated gene of the invention.  
 XX Sequence 96596 BP; 17605 A; 24295 C; 25661 G; 19918 T; 0 U; 9117 Other;  
 Query Match Score 163.4; DB 10; Length 96596;  
 Best Local Similarity 87.6%; Pred. No. 6.6e-27; Mismatches 26; Indels 1; Gaps 1;  
 Matches 190; Conservative 0; Mismatches 26; Indels 1; Gaps 1;

QY 1 GAAATGGACGATCTCTGGTCAACCTCAGGCCCTCCAGTAGCTGGATTACAGGC 60  
 DB 76410 GCAGTGCGGTGATCTCGGTCAACTCCACCTCCGGTAGCTGGATTACAGGC 76469  
 QY 61 ATGCCAACACGCCGGTAATTGGTAACTTGTATAGTAGAGACGGGTCCATGTT 120  
 DB 76470 ATGCCAACACGCCGGTAATTGGTAACTTGTATAGTAGAGACGGGTCCATGTT 76528  
 QY 121 GGTCAGGGCTGGTCTGAACCTCAAGGTATCCGGTATCACCCTCCAAACT 180  
 DB 76529 GGCCAAAGCAGGTCTGAACCTCAACCTCAGGATCTGGCCTCCAAAGT 76588  
 QY 181 GCTTGGATTACAGGGTGAACGGCCAACGGGTCAAGCTG 217  
 DB 76589 GCTGGATTACAGGGATAGCCACGGTGCCTGGGACCTG 76625

RESULT 1.3  
 ADA02720 Human NFATC1 carcinoma associated gene, SEQ ID NO:1228.  
 ID ADA02720 standard; DNA; 96597 BP.  
 XX ADA02720;  
 XX 06-NOV-2003 (first entry)  
 XX DE Human NFATC1 carcinoma associated gene, SEQ ID NO:1228.  
 XX KW Human; carcinoma; associated; oncogene; carcinoma; cancer; breast;  
 KW prostate; lymphoma; leukaemia; cytostatic; gene therapy; drug screening;  
 KW gene; ds.  
 XX Homo sapiens.  
 XX WO2003057146-A2.  
 XX PD 17-JUL-2003.  
 XX PF 26-DEC-2002; 2002WO-US041414.  
 XX PR 26-DEC-2001; 2001US-00035832.  
 PA (SAGR-) SAGRES DISCOVERY.  
 XX Morris DW;  
 XX DR 2003-587068/55.  
 XX PT New recombinant nucleic acid encoding carcinoma associated protein, useful for preparing compositions for treating carcinomas.  
 PS Claim 1; SEQ ID NO 1238; 245pp; English.

The invention relates to recombinant carcinoma associated (CA) nucleic acid sequences from mouse and human (ADA0142-ADA0309A), and to recombinant carcinoma associated proteins (CAP) encoded by them. The invention also encompasses expression vectors and host cells comprising a CA nucleic acid, a polypeptide (especially an antibody) that specifically binds to the protein, and a biochip comprising CA nucleic acid or fragments thereof. The sequence of the invention were identified using oncogenic retroviruses, which insert into the genome of the host organism at random. Many of these do not carry transduced host oncogenes or pathogenic trans-acting viral genes, meaning that cancer incidence is a direct consequence of the effects of proviral integration into host protooncogenes. The CA nucleic acid sequences can be used to diagnose carcinoma (especially breast cancer, prostate cancer, lymphoma or

CC leukaemia) or a propensity to carcinoma by determination of the sequence of a CA gene, or by determination of CA gene expression in particular tissues. CA nucleic acids, proteins and antibodies are also useful as therapeutic agents and in screening and evaluating drug candidates. The present sequence represents a specifically claimed human CA nucleic acid sequence of the invention. Note: The complete sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [ftp.wipo.int/pub/published\\_pct\\_sequences](http://wipo.int/pub/published_pct_sequences).

XX Sequence 96597 BP; 17605 A; 24295 C; 25662 G; 19918 T; 0 U; 9117 Other;  
 SQ Query Match Score 163.4; DB 9; Length 96597;  
 Best Local Similarity 87.6%; Pred. No. 6.6e-27;  
 Matches 190; Conservative 0; Mismatches 26; Indels 1; Gaps 1;

QY 1 GATATGGCGATCTCTGGTCAACTCAGCTAACCTCAGGTTGGATTACAGGC 60  
 DB 76411 GCACTGGCTGTGATCTGGGTCACTGCACCTCCGGTACGGTGGATTACAGGC 76470  
 QY 61 ATGGGCCACCAACGCCGGCTTAATTGGTATCCTTTAGTAGAGGGCTTCCTCATGTT 120  
 DB 76471 ATGGACCAACGCCGGCTTAATTGGTATCCTTTAGTAGAGGGGTTGGCATGTT 76529

QY 121 GGTCAGGGCTGGTCTGAACCTCAAGGTATCCGGTATCACCCTCCAAACT 180  
 DB 76530 GGCGAAGGATGGTCTGGAAACTCCGACCTCAGGATCGGCTCTCCAAAGT 76589  
 QY 181 GCTTGGATTACAGGGTGAACGGCCAACGGGTCAAGCTG 217  
 DB 76590 GCTGGGATTACAGGGATAGCCACGGTGCCTGGCTGT 76625

RESULT 14  
 ADB2458 standard; DNA; 96597 BP.  
 XX AC ADB72458;  
 XX DT 04-DEC-2003 (first entry)  
 XX DE Human NFATC1 gene.  
 XX KW human; ds; cytostatic; gene therapy; vaccine; carcinoma; lymphomas; cancer; neoplasm; adenocarcinoma; sarcoma; gene.  
 XX OS Homo sapiens.  
 XX PN WO2003008583-A2.  
 XX PD 30-JAN-2003.  
 XX PP 26-DEC-2001; 2001WO-US051291.  
 XX PR 02-MAR-2001; 2001US-00798586.  
 XX PR 23-OCT-2001; 2001US-0004113.  
 XX PR 08-NOV-2001; 2001US-0052482.  
 XX PR 30-NOV-2001; 2001US-0097722.  
 XX PR 20-DEC-2001; 2001US-0034650.

PA (SAGR-) SAGRES DISCOVERY.  
 XX Morris DW, Engelhardt BK;  
 XX WPI; 2003-233337/23.  
 XX PR New recombinant nucleic acid, useful for treating carcinomas, lymphomas, cancers, neoplasm, adenocarcinoma, or sarcomas.  
 XX PS Claim 1; SEQ ID NO 286; 2304pp; English.  
 XX CC The invention relates to a novel recombinant nucleic acid comprising a nucleotide sequence selected from any of the 660 sequences fully defined

CC in the specification. A polynucleotide of the invention has cytostatic  
 CC activity, and may have a use in gene therapy, or in a vaccine. The  
 CC recombinant nucleic acids and polypeptides are useful for treating  
 CC carcinomas, e.g. lymphomas, cancers, neoplasms, adenocarcinoma, and  
 CC sarcomas. The present sequence represents a human gene of the invention.  
 XX

SQ Sequence 96597 BP; 17605 A; 24295 C; 25662 G; 19918 T; 0 U; 9117 Other;

Query Match 36.6%; Score 163.4; DB 10; Length 96597;  
 Best Local Similarity 87.6%; Pred. No. 6.6e-27;  
 Matches 190; Conservative 0; Mismatches 26; Indels 1; Gaps 1;

QY 1 GTAAATGGCACGATCTCTGCTCACTGCAACTCAGCCTCCCGTAGCTGGGATTACAGGC 60

Db 76411 GCAGTGGCCTGATCTCGGTCACTGCAACTCCACCTCCGGTACAGTCAGGC 76470

QY 61 ATGCCAACACAGGCCGGTAATTGTATCTTTAGTAGAGACGGCTTCCCATTT 120

Db 76471 ATGZACCACCAACGCCGGCTTAATTGTA-ATTTAGTAGAGATGGGTTTGCCATT 76529

QY 121 GGTCAGGGCTGGTCTGAACCTCAACCTCAAGGTATCCGCCGCTCTGCCCTCCAAAGT 180

Db 76530 GGCAAGCAGGTCTGAATGCCAACCTCAAGGTATCCGCCGCTCCAAAGT 76589

QY 181 GCTAGGATACAGGGTGAACGCCACGGCTCAGCTG 217

Db 76590 GCTGGGATACAGGGATAGGCCACCGTGCCTGGCTG 76626

RESULT 15  
 AAD53223\_4  
 Continuation (5 of 5) of AAD53223 from base 400001 (Human chromosome 3 p-arm breakpoint  
 WP Sequence split into 5 fragments LOCUS AAD53223 Accession Ad53223

WP	Fragment Name	Begin	End
WP	AAD53223_0	1	110000
WP	AAD53223_-1	100001	210000
WP	AAD53223_-2	200001	310000
WP	AAD53223_-3	300001	410000
WP	AAD53223_-4	400001	487980

Query Match 36.5%; Score 162.8; DB 8; Length 87980;

Best Local Similarity 88.9%; Pred. No. 8.9e-27;  
 Matches 176; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 23 CTGCACCTAGCCCTCCCGTAGCTGGGATTACAGGATGCGCACATGCTGGCTAA 82

Db 33281 CTTCTACTCTAGGCTCCGAGTAGGATACAGGATGCGCACATGCTGGCTAA 33340

QY 83 TTGTGATCTTTAGTAGAGACGGCTCTCCATGTTGCTAGGTGCTGGCTTCGAACCTC 142

Db 33341 TTGTGATCTTTAGTAGAGACGGCTCTCCATGTTGCTGGCTTCGAACCTC 33400

QY 143 AAACCTCAAGTGATCCGGCCGCTGGCTCCAAAGTGCTAGGATTACAGGGCTGACCC 202

Db 33401 TGACCTTATGTATGCCCTCCGCTGGCTCCAAAGTGCTGGCTTCGAACCTC 33460

QY 203 ACCGGCTAGCTGGAA 220

Db 33461 AATGGCCAGCCAGGA 33478

Search completed: January 15, 2005, 17:06:20  
 Job time : 364 secs

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SUMMARIES									
Result No.	Score	Query Match	Length	DB ID	Description				
C 1	162.2	36.4	8220	4	US-09-797-908-3	Sequence 3, Appli			
C 2	160	35.9	382	4	US-09-513-999C-32874	Sequence 32B4, A			
C 3	158.8	35.6	84495	3	US-09-197-006-3	Sequence 3, Appli			
C 4	151.8	35.4	462	4	US-09-621-976-14372	Sequence 14372, A			
C 5	157.4	35.3	70000	4	US-09-851-996-3	Sequence 3, Appli			
C 6	156.4	35.1	1811	1	US-08-848-232-1	Sequence 1, Appli			
C 7	154	34.5	63000	4	US-09-780-17-18	Sequence 18, Appli			
C 8	153.4	34.4	354	4	US-09-121-976-8798	Sequence 8798, Appli			
C 9	153.4	34.4	373	4	US-09-621-976-14426	Sequence 14426, A			
C 10	153.4	34.4	841	5	PCT-US93-06251-80	Sequence 80, Appli			
C 11	153.4	34.4	841	5	PCT-US93-06251-81	Sequence 81, Appli			
C 12	153.4	34.4	66933	4	US-09-544-998B-11	Sequence 11, Appli			
C 13	153.4	34.4	66933	4	US-09-543-771-11	Sequence 11, Appli			
C 14	153.4	34.4	72049	4	US-09-544-998B-9	Sequence 9, Appli			
C 15	153.4	34.4	72049	4	US-09-543-771-9	Sequence 9, Appli			
C 16	153.2	34.3	609	3	US-09-385-982-237	Sequence 237, Appli			
C 17	153.2	34.3	1371	4	US-09-023-655-986	Sequence 986, Appli			
C 18	153.2	34.3	343	3	US-08-323-443B-1	Sequence 1, Appli			
C 19	153.2	34.3	53526	3	US-08-658-136-2	Sequence 2, Appli			
C 20	153.2	34.3	53577	3	US-08-658-136-1	Sequence 1, Appli			
C 21	153	34.3	282	1	US-08-133-229-8	Sequence 8, Appli			
C 22	153	34.3	283	4	US-08-579-445-26	Sequence 26, Appli			
C 23	152.8	34.3	2839	3	US-09-061-702-1	Sequence 1, Appli			
C 24	152.8	34.3	2839	4	US-09-748-451-1	Sequence 1, Appli			
C 25	152.8	34.3	168174	4	US-10-071-411A-63	Sequence 63, Appli			
C 26	152.8	34.3	168273	4	US-10-071-411A-63	Sequence 2, Appli			
C 27	151.8	34.0	21721	4	US-09-269-939A-41	Sequence 41, Appli			

Patent No. 6783961  
 FILE REFERENCE: 59.US2.REG  
 CURRENT APPLICATION NUMBER: US/09/513, 999C  
 CURRENT FILING DATE: 2000-02-24  
 PRIOR APPLICATION NUMBER: US 60/122, 487  
 PRIORITY FILING DATE: 1999-02-26  
 NUMBER OF SEQ ID NOS: 36681  
 SOFTWARE: Patent .pm  
 SEQ ID NO: 32874  
 LENGTH: 382  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 FEATURE: misc\_feature  
 LOCATION: 283 ..  
 OTHER INFORMATION: n=a, g, c or t  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: 284 ..  
 OTHER INFORMATION: n=a, g, c or t  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: 311 ..  
 OTHER INFORMATION: m=a or c  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: 319 ..  
 OTHER INFORMATION: k=g or t  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: 321 ..  
 OTHER INFORMATION: k=g or t  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: 352 ..  
 OTHER INFORMATION: s=g or c  
 US-09-513-999C-32874

Query Match 35.9%; Score 160; DB 4; Length 382;  
 Best Local Similarity 85.3%; Pred. No. 2.2e-32;  
 Matches 186; Conservative 2; Mismatches 29; Indels 1; Gaps 1;

Qy 1 GTAATGGCACGATCTCTGTCACTGCAACTCGCCAGTAGCTGGATTACAGGC 60  
 Db 344 GTAATGGCGGATCTGGTCACAGAACCTCCCTGGGTAGCTGGATTACAGGC 285

Qy 61 ATGCCCAACAGGGCTTAATTGTATCTTTAGTAGAGCGGGTCCCTCATGT 120  
 Db 284 NNGTCCACAGGCCAGCTAAATTGTAT-TTTAGTAGAGCACGGTTTCCCATTT 226

Qy 121 GCTAGGATTAAGGGTGTCTGAACCTAGGTATCCCGCGCTCCSCCTCCAAAGT 180  
 Db 225 GGTAGGGTGTCTGAAGTCCCACCTAGGGATCCGGCCACCTCGGCTG 166  
 Db 165 GCTGGGATTAAGGGTGTCTGAACCTAGGTATCCGGCCACCTCGGCTG 128

RESULT 3  
 US-09-797-906-3/c  
 Sequence 3, Application US/09797906  
 Patent No. 6329188

GENERAL INFORMATION:  
 APPLICANT: Zianghe YAN, Karen A. KETCHUM, Valentine DIFRANCESCO, Eileen M. BEASLEY  
 TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,  
 TITLE OF INVENTION: NUCLEAR ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND  
 FILE REFERENCE: CL00115CIP

CURRENT APPLICATION NUMBER: US/09/797, 906  
 CURRENT FILING DATE: 2001-03-05  
 NUMBER OF SEQ ID NOS: 5  
 SOFTWARE: FastSEQ for Windows Version 4.0

Patent No. 3  
 LENGTH: 84495  
 TYPE: DNA  
 ORGANISM: Human  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: (1)..(84495)  
 OTHER INFORMATION: n = A,T,C or G  
 US-09-797-906-3

Query Match 35.6%; Score 158.8; DB 3; Length 84495;  
 Best Local Similarity 88.7%; Pred. No. 3.4e-31;  
 Matches 172; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

Qy 23 CTCGAACTCAGCTCCCTCCAGTAGCTGGATTACAGGCTACGCCACCGCCGGCTRA 82  
 Db 46895 CTCTGCCCTCAGCTACCGAATGAGCTGGATTAGAGCGGTGGCACCACGCCGGCTAA 46837

Qy 83 TTTTGATCTTTAGTAGAGACGGTTCCTCATGGTGGTGGCTGGAACTTC 142  
 Db 46836 TTTCATATTTTTAGTAGAGCGGGTTTCATGGTGGTGGCTGGAACTTC 46777

Qy 143 AACCTCAGGTATCCGCCCTGGCTCGGCCTCCAAAGTGTAGGATTACAGGGTGGCC 202  
 Db 46776 CAACTCAGTGTGTCGCCCTCGGCCTCAAGTGTGGATTACAGGGTGGCC 46717

Qy 203 ACCGGCTCAGGCT 216  
 Db 46716 ACCGGGCCGGCT 46703

RESULT 4  
 US-09-621-976-14372/C  
 Sequence 14372, Application US/09621976  
 Patent No. 6639063

GENERAL INFORMATION:  
 APPLICANT: Dunas Milne Edwards, J.B.  
 ATTORNEY: Jobert, S.  
 ATTORNEY: Giordano, J.Y.  
 TITLE OF INVENTION: EST-8 and Encoded Human Proteins.

FILE REFERENCE: GENSET-054PH2

CURRENT APPLICATION NUMBER: US/09/621, 976

CURRENT FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 19335

SOFTWARE: Patent .pm

SEQ ID NO: 14372

Length: 462;

Query Match 35.4%; Score 158; DB 4;  
 Best Local Similarity 67.8%; Pred. No. 7.9e-32;  
 Matches 236; Conservative 0; Mismatches 110; Indels 2; Gaps 1;

Qy 29 CCTAGGCTCCCGAGTAGCTGGATTACAGGATGCCACACGGCTAATTTGT 88  
 Db 369 CCTAGGCTCCCGAGTAGCTGGATTATAGGATGGACCCAGGCTGGCTAATTTGT 310

Qy 89 ATCTTTAGTAGAGAGGGCTCCATGTTGGCTGGATTACAGGCTGGCTAATTTGT 148  
 Db 309 TATGTTAGTAGAGATGGGTCAACCTCTGTTCAACTCTGTCACCTGACCT 250

Qy 149 CAGGTGATTCGGCCGGCTTCGGCTCCAAAGTGTAGGATTAAGGGCTGGCTAATTTGT 88

Db 249 CAGGTGATTCACCTGGCTGGCTCCAAAGTGTGGATTACAGGATGGCTGGCTAATTTGT 190

Qy 209 CTAGGCTGGGACACCTTCTTACATCTCAAGGCTAGAATGCTTATGAAACGAA 268

Db 189 CCCAGCCAATTATATTAATTTTAAAAATTACTGTTTAAAAA-ATTATGAAAGTAAAC 132

Qy 269 AAAAGAATTATAAGAGTAATTATAAGAAACACTCATTTCTCCCAAAGAGGCCAGA 328

RESULT 5  
US-09-851-896-3/c  
 Sequence 3, Application US/09851896  
 i Patent No. 6410325  
 GENERAL INFORMATION:  
 i APPLICANT: C. Frank Bennett  
 i APPLICANT: Susan M. Freier  
 i APPLICANT: Andrew T. Watt  
 i TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP VI (CR2+-INDEPENDENT)  
 i FILE REFERENCE: RTS-0220  
 CURRENT APPLICATION NUMBER: US/09/851,896  
 i CURRENT FILING DATE: 2001-05-08  
 i NUMBER OF SEQ ID NOS: 89  
 i SEQ ID NO 3  
 LENGTH: 70000  
 i TYPE: DNA  
 i ORGANISM: Homo sapiens  
 i FEATURE:  
 us-09-851-896-3

Query Match 35.3%; Score 157.4; DB 4; Length 70000;  
 Best Local Similarity 86.9%; Pred. No. 7.4e-31;  
 Matches 173; Conservative 0; N mismatches 26; Indels 0; Gaps 0;

Qy 83 TTTCGTATCTTTAGTA GAGACGGCTTCCCATGTTGTCAAGCTGTCTGAACRTC 142  
 Db 41118 TTTCGTATTTAGTA GAGATGGTTCTCATGTGTCACTGGCTGAACTCC 41059

Qy 143 AAACCTCAAGTGATCGGCCCTCCGCTCCAAAGTGCTAGGATTACAGGCCTGAGCC 202  
 Db 41058 CGACCTCAAGTGATCGGCCACCTCAAGCTTCCAAAGTGTTGGATTACAGGCCTGAGAC 40999.

Qy 203 ACCGGCTCACCCCTGGAA 221  
 Db 40998 ACCGGCCCAAGCCAGAAA 40980

RESULT 6  
US-09-848-252-1  
 Sequence 1, Application US/08848252  
 i Patent No. 5804177  
 GENERAL INFORMATION:  
 i APPLICANT: Humphries, Keith R.  
 i TITLE OF INVENTION: METHOD OF USING CD24 AS A CELL MARKER  
 i NUMBER OF SEQUENCES: 4  
 CORRESPONDENCE ADDRESS:  
 i ADDRESSEE: Berekin & Parr  
 i STREET: 40 King Street West  
 i CITY: Toronto  
 i STATE: Ontario  
 i COUNTRY: Canada  
 i ZIP: M5H 3Y2  
 COMPUTER READABLE FORM:  
 i MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 i APPLICATION NUMBER: US/08/848,252  
 i FILING DATE: 29-APR-1997  
 i CLASSIFICATION: 435

RESULT 7  
US-09-780-172-18/c  
 Sequence 18, Application US/09780172  
 i Patent No. 6607116  
 GENERAL INFORMATION:  
 i APPLICANT: Robert McKay  
 i APPLICANT: Susan M. Freier  
 i APPLICANT: Jacqueline Wyatt  
 i TITLE OF INVENTION: ANTISENSE MODULATION OF CASEIN KINASE 2-ALPHA EXPRESSION  
 i FILE REFERENCE: RTS-0159  
 i CURRENT APPLICATION NUMBER: US/09/780,172  
 i CURRENT FILING DATE: 2001-02-08



i TYPE: nucleic acid  
 i STRANDEDNESS: double  
 i TOPOLOGY: linear  
 i MOLECULE TYPE: DNA (genomic)  
 PCT-US93-06251-80

Query Match 34.4%; Score 153.4; DB 5; Length 841;  
 Best Local Similarity 81.8%; Pred. No. 1..5e-30;  
 Matches 189; Conservative 0; Mismatches 41; Indels 1; Gaps 1;

Qy 23 CTGCAACCTAGCCTCCAGTAGTGGATTACAGGCATGCCAACAGCGGTAA 82  
 Db 250 CTCTGCTCTAGCCTCCGGTAGTGGATTACAGGATGCCAACACCGGGTAA 191  
 Qy 83 TTTCGTATCTTTAGTAGAGACGGGTTCCTCCATGTTGCTCGAACITC 142  
 Db 190 TTTCGTAT-TTTAGTAAGATGGTTTACCATGTTGCTCGAACITC 132  
 Qy 143 AACCTCTAGTGTATGGCCCTCGGCCCTCCAAAAGTGTAGGATTACAGGCTGAGCC 202  
 Db 131 CGACCTCTAGTGTATGCCCTCCAAAAGTGTGGATTACAGGCTGAGCC 72

Qy 203 ACCGGCTCAACCTGGAAACCTTTCTACATCTTCAAGTGTAGAAT 253  
 Db 71 ACCGGACCGCCCTGCCCTGCTGTGTTTGATCACAGGTCAACTAAT 21

RESULT 11

PCT-US93-06251-81/c

Sequence 81, Application PC/TUS9306251

GENERAL INFORMATION:

APPLICANT: Wickstrom, Eric and Rife, Jason P.

TITLE OF INVENTION: Trivalent Synthesis of Oligonucleotides Containing Arylphosphonates

NUMBER OF SEQUENCES: 93

CORRESPONDENCE ADDRESS:

ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER

STREET: 400 Garden City Plaza

CITY: Garden City

STATE: NY

ZIP: 11530

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patient In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/TUS93/06251

FILING DATE: 19930630

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: DiGilio, Frank S.

REGISTRATION NUMBER: 31,346

REFERENCE/DOCKET NUMBER: 8586

TELECOMMUNICATION INFORMATION:

TELEPHONE: 516-742-4343

TELEX: 230 901 SANS UR

INFORMATION FOR SEQ ID NO: 81:

SEQUENCE CHARACTERISTICS:

LENGTH: 841 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

PCT-US93-06251-81

Query Match 34.4%; Score 153.4; DB 5; Length 841;

Best Local Similarity 81.8%; Pred. No. 1..5e-30;

Matches 189; Conservative 0; Mismatches 41; Indels 1; Gaps 1;

Qy 23 CTGCAACCTAGCCTCCAGTAGTGGATTACAGGATGCCAACACCGGGTAA 82

Db 250 CTCTGCTCTAGCCTCCGGTAGTGGATTACAGGATGCCAACACCGGGTAA 191

Db 250 CTCTGCTCTAGCCTCCAGTAGTGGATTACAGGATGCCAACACCGGGTAA 191

Qy 83 TTTCGTATCTTTAGTAGAGACGGGTTCCTCCATGTTGCTCGAACITC 142

Db 190 TTTCGTAT-TTTAGTAAGATGGTTTACCATGTTGCTCGAACITC 132

Qy 143 AACCTCTAGTGTATGGCCCTCGGCCCTCCAAAAGTGTAGGATTACAGGCTGAGCC 202

Db 131 CGACCTCTAGTGTATGCCCTCCAAAAGTGTGGATTACAGGCTGAGCC 72

Qy 203 ACCGGCTCAACCTGGAAACACCTTTCTACATCTTCAAGTGTAGAAT 253

Db 71 ACCGGACCGCCCTGCCCTGCTGTGTTTGATCACAGGTCAACTAAT 21

RESULT 12

US-09-544-398B-11

Sequence 11, Application US/09544398B

PATENT NO. 677061

GENERAL INFORMATION:

APPLICANT: Carilli, John P.

REKEK, Robert R.

JOHNSON, Mark L.

TITLE OF INVENTION: High bone mass gene of 11q13.3

FILE REFERENCE: 032796-013

CURRENT APPLICATION NUMBER: US/09/544,398B

CURRENT FILING DATE: 2002-06-10

PRIOR APPLICATION NUMBER: US 09/229,319

PRIOR FILING DATE: 1999-01-13

PRIOR APPLICATION NUMBER: US 60/071,449

PRIOR FILING DATE: 1998-01-13

PRIOR APPLICATION NUMBER: US 60/105,511

PRIOR FILING DATE: 1998-10-23

NUMBER OF SEQ ID NO: 641

SOFTWARE: Fastseq for Windows Version 4.0

SEQ ID NO: 11

LENGTH: 66933

TYPE: DNA

ORGANISM: Homo sapiens

US-09-544-398B-11

Query Match 34.4%; Score 153.4; DB 4; Length 66933;

Best Local Similarity 82.9%; Pred. No. 7.9e-30;

Matches 175; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

Qy 23 CTGGAAACCTAGCCTCCAGTAGTGGATTACAGGATGCCACCAAGCGGTAA 82

Db 52539 CTCTGCTCTAGCTCCAGTAGTGGATTACAGGATGCCACCAAGCGGTAA 52598

Qy 83 TTTCGTATCTTTAGTAGAGACGGGTTCCTCCATGTTGCTCGAACITC 142

Db 52599 TTTCGTATTTAGTAGAGACGGGTTCCTCCATGTTGCTCGAACITC 52658

Qy 143 AACCTCTAGTGTATGGCCCTCGGCCCTCCAAAAGTGTAGGATTACAGGCTGAGCC 202

Db 52659 TGACCTAGCTAGCCTGGATCCAGGATGCCACCAAGCGGTAA 52218

Qy 203 ACCGGCTCAACCTGGAAACACCTTTCTTA 233

Db 52719 ACCGGCCGGCTGAGTTTCCCTTATGA 52749

RESULT 13

US-09-543-771-11

Sequence 11, Application US/09543771

PATENT NO. 6780609

GENERAL INFORMATION:

APPLICANT: John P. Carnilli et al.

TITLE OF INVENTION: THE HIGH BONE MASS GENE OF 11q13.3

FILE REFERENCE: 032796-013

CURRENT APPLICATION NUMBER: US/09/543,771

CURRENT FILING DATE: 2000-04-05  
; EARLIER APPLICATION NUMBER: US 09/229,319  
; EARLIER FILING DATE: 1999-01-13  
; EARLIER APPLICATION NUMBER: US 60/071,449  
; EARLIER FILING DATE: 1998-01-13  
; EARLIER APPLICATION NUMBER: US 60/105,511  
; EARLIER FILING DATE: 1998-10-23  
; SEQ ID NO: 11  
; LENGTH: 66933  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-543-711-11

Query Match 34.4%; Score 153.4; DB 4; Length 66933;  
Best Local Similarity 82.9%; Pred. No. 7.9e-30; Indels 0; Gaps 0;  
Matches 175; Conservative 0; Mismatches 36; Delins 0; Gaps 0;  
; Sequence 9, Application US/09543771  
; Patent No. 6780609  
; GENERAL INFORMATION:  
; APPLICANT: John P. Carulli et al.  
; TITLE OF INVENTION: THE HIGH BONE MASS GENE OF 11q13.3  
; FILE REFERENCE: 032796-013  
; CURRENT FILING DATE: US/09/543,771  
; EARLIER APPLICATION NUMBER: US 09/229,319  
; EARLIER FILING DATE: 1999-01-13  
; EARLIER APPLICATION NUMBER: US 60/071,449  
; EARLIER FILING DATE: 1998-01-13  
; EARLIER APPLICATION NUMBER: US 60/105,511  
; EARLIER FILING DATE: 1998-10-23  
; NUMBER OF SEQ ID NOS: 62  
; SEQ ID NO: 9  
; LENGTH: 72049  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (B356), (8385), (38585)  
; OTHER INFORMATION: Identity of nucleotide sequences at the above locations are unkno

RESULT 15  
US-09-543-771-9  
; Sequence 9, Application US/09543771  
; Patent No. 6780609  
; GENERAL INFORMATION:  
; APPLICANT: Carulli, John P.  
; APPLICANT: Little, Randall D.  
; APPLICANT: Recker, Robert R.  
; APPLICANT: Johnson, Mark L.  
; TITLE OF INVENTION: High bone mass gene of 11q13.3  
; FILE REFERENCE: 032796-013  
; CURRENT FILING DATE: 2002-06-10  
; PRIOR APPLICATION NUMBER: US/09/544,398B  
; PRIOR FILING DATE: 1999-01-13  
; PRIOR APPLICATION NUMBER: US 60/071,449  
; PRIOR FILING DATE: 1998-01-13  
; PRIOR APPLICATION NUMBER: US 60/105,511  
; PRIOR FILING DATE: 1998-10-23  
; NUMBER OF SEQ ID NOS: 641  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO: 9  
; LENGTH: 72049  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (B356), (8385), (38585)  
; OTHER INFORMATION: Identity of nucleotide sequences at the above locations are unkno

Query Match 34.4%; Score 153.4; DB 4; Length 72049;  
Best Local Similarity 82.9%; Pred. No. 8.1e-30; Indels 0; Gaps 0;  
Matches 175; Conservative 0; Mismatches 36; Delins 0; Gaps 0;  
; Sequence 9, Application US/09543771  
; Patent No. 6780609  
; GENERAL INFORMATION:  
; APPLICANT: John P. Carulli et al.  
; TITLE OF INVENTION: THE HIGH BONE MASS GENE OF 11q13.3  
; FILE REFERENCE: 032796-013  
; CURRENT FILING DATE: US/09/543,771  
; EARLIER APPLICATION NUMBER: US 09/229,319  
; EARLIER FILING DATE: 1999-01-13  
; EARLIER APPLICATION NUMBER: US 60/071,449  
; EARLIER FILING DATE: 1998-01-13  
; EARLIER APPLICATION NUMBER: US 60/105,511  
; EARLIER FILING DATE: 1998-10-23  
; NUMBER OF SEQ ID NOS: 62  
; SEQ ID NO: 9  
; LENGTH: 72049  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (B356), (8385), (38585)  
; OTHER INFORMATION: Identity of nucleotide sequences at the above locations are unkno

Query Match 34.4%; Score 153.4; DB 4; Length 72049;  
Best Local Similarity 82.9%; Pred. No. 8.1e-30; Indels 0; Gaps 0;  
Matches 175; Conservative 0; Mismatches 36; Delins 0; Gaps 0;  
; Sequence 9, Application US/09543771  
; Patent No. 6780609  
; GENERAL INFORMATION:  
; APPLICANT: Carulli, John P.  
; APPLICANT: Little, Randall D.  
; APPLICANT: Recker, Robert R.  
; APPLICANT: Johnson, Mark L.  
; TITLE OF INVENTION: High bone mass gene of 11q13.3  
; FILE REFERENCE: 032796-013  
; CURRENT FILING DATE: 2002-06-10  
; PRIOR APPLICATION NUMBER: US/09/544,398B  
; PRIOR FILING DATE: 1999-01-13  
; PRIOR APPLICATION NUMBER: US 60/071,449  
; PRIOR FILING DATE: 1998-01-13  
; PRIOR APPLICATION NUMBER: US 60/105,511  
; PRIOR FILING DATE: 1998-10-23  
; NUMBER OF SEQ ID NOS: 641  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO: 9  
; LENGTH: 72049  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (B356), (8385), (38585)  
; OTHER INFORMATION: Identity of nucleotide sequences at the above locations are unkno

Query Match 34.4%; Score 153.4; DB 4; Length 72049;  
Best Local Similarity 82.9%; Pred. No. 8.1e-30; Indels 0; Gaps 0;  
Matches 175; Conservative 0; Mismatches 36; Delins 0; Gaps 0;  
; Sequence 9, Application US/09543771  
; Patent No. 6780609  
; GENERAL INFORMATION:  
; APPLICANT: John P. Carulli et al.  
; TITLE OF INVENTION: THE HIGH BONE MASS GENE OF 11q13.3  
; FILE REFERENCE: 032796-013  
; CURRENT FILING DATE: US/09/543,771  
; EARLIER APPLICATION NUMBER: US 09/229,319  
; EARLIER FILING DATE: 1999-01-13  
; EARLIER APPLICATION NUMBER: US 60/071,449  
; EARLIER FILING DATE: 1998-01-13  
; EARLIER APPLICATION NUMBER: US 60/105,511  
; EARLIER FILING DATE: 1998-10-23  
; NUMBER OF SEQ ID NOS: 62  
; SEQ ID NO: 9  
; LENGTH: 72049  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (B356), (8385), (38585)  
; OTHER INFORMATION: Identity of nucleotide sequences at the above locations are unkno

Search completed: January 15, 2005, 18:23:05  
Job time : 78 sec

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: January 15, 2005, 18:21:58 ; Search time 385 Seconds  
(without alignments)

6656.276 Million cell updates/sec

Title: US-10-009-579-5\_COPY\_3115\_3560

Perfect score: 446

Sequence: 1 gtaatggcacatctgtct...ctggaaaggttctctgccttgt 446

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4300275 seqs, 2872944193 residues

Total number of hits satisfying chosen parameters: 8600550

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Listing first 45 summaries

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 21: /cgcn2\_6\_ptodata/2/pubpna/us06\_pubcomb.seq/\*

## RESULT 1

US-10-009-579-5

; Sequence 5, Application US/10009579  
 ; Publication No. US20020156041A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Leijde, Lou F.M.H.  
 ; APPLICANT: Ruiters, Marcel H.J.  
 ; APPLICANT: McNaughlin, Pamela M.J.  
 ; APPLICANT: Hamsemen, Martin C.  
 ; APPLICANT: Molten V.d., Henk  
 ; APPLICANT: Terpstra, Peter  
 ; APPLICANT: Dokter, Willem H.A.  
 ; TITLE OF INVENTION: Non-squamous epithelium-specific transcription  
 ; FILE REFERENCE: P52075US0  
 ; CURRENT APPLICATION NUMBER: US/10/009,579  
 ; CURRENT FILING DATE: 2002-03-26  
 ; PRIOR APPLICATION NUMBER: EP 00200728.4  
 ; PRIOR FILING DATE: 2000-03-01  
 ; PRIORITY APPLICATION NUMBER: PCT/NL01/00166  
 ; NUMBER OF SEQ ID NOS: 5  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 5  
 ; LENGTH: 4282  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: (1)-(4282)  
 ; OTHER INFORMATION: /note="EGP-2 promotor sequence from -3967 to +315"

US-10-009-579-5

Query Match 100.0%; Score 446; DB 13;  
 Best Local Similarity 100.0%; Pred. No. 6.-e-98;  
 Matches 446; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	446	100.0	4282	13	US-10-009-579-5 Sequence 5, Appli Sequence 7667, Appli
2	169.6	38.0	4388	10	US-09-764-891-647 Sequence 604, Appli
3	169.2	37.9	3252	16	US-10-108-260A-604 Sequence 34, Appli
C 4	161.66	37.2	26874	15	US-10-004-113-34 Sequence 4, Appli
C 5	165.8	37.2	289	14	US-10-115-278-4 Sequence 4, Appli
C 6	165.8	37.2	289	18	US-10-162-966-4 Sequence 15, Appli
C 7	165.8	37.2	291	15	US-10-229-058B-15 Sequence 70, Appli
C 8	164.4	36.9	133300	18	US-10-331-053-70 Sequence 165142, Sequence 165143, Sequence 165142, Sequence 165143,
9	163.6	36.7	912	13	US-10-027-632-165142 Sequence 165142, Sequence 165143, Sequence 165142, Sequence 165143,
10	163.6	36.7	912	13	US-10-027-632-165143 Sequence 165142, Sequence 165143, Sequence 165142, Sequence 165143,
11	163.6	36.7	912	15	US-10-027-632-165142 Sequence 165142, Sequence 165143, Sequence 165142, Sequence 165143,
12	163.6	36.7	912	15	US-10-027-632-165143 Sequence 165142, Sequence 165143, Sequence 165142, Sequence 165143,

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.



Db 22835 GCAGTGGCATGATCTAOGCTCACTCCAACTTCAGCCTCTCGAGTAGCTGGATTACAGGC 22776  
 Qy 61 ATGCCAACACGCCGGCTTAATTGTATCTTTAGTAGAGACGGCTCCCTCATGTT 120  
 Db 22775 ACGTACCAACCGCTGGTAAATTGTGTTATTAGTAGAGACGGTTACCATGTT 22716  
 Qy 121 GGTAGGGTGTTGTAACTCAAACTCAGGTATCAGCCGCTCGGCCTCCAAAGT 180  
 Db 22715 GGCCRAGCTGCTCAACTCTGACCTCACCTCCCTACSCCTCCAACCT 22656  
 Qy 181 GCTAGGATTACAGGGTAGCCACCGCTCAGCTGGAAACACCTTCTTAATCT 238  
 Db 22655 ACTGGGATACAAGGTAGGCCACTGGCCAACTGAAGCCTTAATACATT 22598

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RESULT 5  
 US-10-115-278-4/c  
 Sequence 4, Application US/10115278  
 Publication No. US20030082644A1  
 GENERAL INFORMATION:  
 APPLICANT: Urnovitz, Howard B.  
 APPLICANT: Schuetz, Ekkehard  
 TITLE OF INVENTION: Chronix Biomedical, Inc.  
 Diagnostic Detection of Nucleic Acids  
 FILE REFERENCE: 018651-000320US  
 CURRENT APPLICATION NUMBER: US/10/115,278  
 CURRENT FILING DATE: 2002-07-09  
 PRIORITY NUMBER: US 60/280,523  
 PRIORITY FILING DATE: 2001-01-30  
 NUMBER OF SEQ ID NOS: 36  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 4  
 LENGTH: 289  
 TYPE: DNA  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence:AluSp consensus  
 US-10-115-278-4

Query Match 37.2%; Score 165.8; DB 18; Length 289;  
 Best Local Similarity 91.2%; Pred. No. 2.1e-30;  
 Matches 176; Conservative 0; Mismatches 17; Indels 0; Gaps 0;  
 Qy 23 CTGAAACCTCAGCTCCCAAGTAGCTGGATTACAGGATGCCCAGGCCGGCTAA 82  
 Db 193 CTCTGGCTCAGCTCCCGAGTAGCTGGATTACAGGATGCCCAGGCCGGCTAA 134  
 Qy 83 TTTTGTATTTTGTAGTAGAGACGGCTTCCTCCATGTTCTGTCAGCTGTCGAACTTC 142  
 Db 133 TTTTGTATTTTGTAGTAGAGACGGCTTCCTCCATGTTCTGTCAGCTGTCGAACTTC 74  
 Qy 143 AACCTCAGTGTAGCCGGCTCCAGGCTTCCTCCAAAGTGCTAGGATTACAGGCC 202  
 Db 73 CGACCTCAGTGTAGCCGGCTCCAGGCTTCCTCCAAAGTGCTGGATTACAGGCC 14  
 Qy 203 ACCGGCTAGCC 215  
 Db 13 ACCGGCCGGCC 1

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RESULT 7  
 US-10-229-058B-15/c  
 Sequence 15, Application US/10229058B  
 Publication No. US20030194718A1  
 GENERAL INFORMATION:  
 APPLICANT: Hirayuki TOMITA, Toshiro SAITO, Masatoshi NARAHARA and  
 APPLICANT: Hirokazu KATO  
 TITLE OF INVENTION: PROBE SEQUENCE DETERMINATION SYSTEM FOR DNA  
 FILE REFERENCE: PH-1629  
 CURRENT APPLICATION NUMBER: US/10/229,058B  
 CURRENT FILING DATE: 2002-08-28  
 NUMBER OF SEQ ID NOS: 35  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 15  
 LENGTH: 291  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 US-10-229-058B-15

Query Match 37.2%; Score 165.8; DB 15; Length 291;  
 Best Local Similarity 91.2%; Pred. No. 2.1e-30;  
 Matches 176; Conservative 0; Mismatches 17; Indels 0; Gaps 0;  
 Qy 23 CTGAAACCTCAGCTCCCAAGTAGCTGGATTACAGGATGCCCAGGCCGGCTAA 82  
 Db 193 CTCTGGCTCAGCTCCCGAGTAGCTGGATTACAGGATGCCCAGGCCGGCTAA 134  
 Qy 83 TTTTGTATTTTGTAGTAGAGACGGCTTCCTCCATGTTCTGTCAGCTGTCGAACTTC 142  
 Db 133 TTTTGTATTTTGTAGTAGAGACGGCTTCCTCCATGTTCTGTCAGCTGTCGAACTTC 74  
 Qy 143 AACCTCAGTGTAGCCGGCTCCAGGCTTCCTCCAAAGTGCTAGGATTACAGGCC 202  
 Db 73 CGACCTCAGTGTAGCCGGCTCCAGGCTTCCTCCAAAGTGCTGGATTACAGGCC 14  
 Qy 203 ACCGGCTAGCC 215  
 Db 13 ACCGGCCGGCC 1

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RESULT 6  
 US-10-762-966-4/c  
 Sequence 4, Application US/10762966  
 Publication No. US20040241712A1  
 GENERAL INFORMATION:  
 APPLICANT: Schuetz, Ekkehard  
 APPLICANT: Urnovitz, Howard B.  
 APPLICANT: Chronix Biomedical, Inc.  
 TITLE OF INVENTION: Diagnostic Detection of Nucleic Acids  
 FILE REFERENCE: 018651-000320US  
 CURRENT APPLICATION NUMBER: US/10/762,966  
 CURRENT FILING DATE: 2004-01-21

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Db          ||||| 13 ACCGCCCCGCC 1
             ; NUMBER OF SEQ ID NOS: 325720
             ; SOFTWARE: FastSEQ for Windows Version 4.0
             ; SEQ ID NO 165142
             ; LENGTH: 912
             ; TYPE: DNA
             ; ORGANISM: Human
             ; US-10-027-632-165142

RESULT 8
; Sequence 70, Application US/10331053
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 59432001100
; CURRENT APPLICATION NUMBER: US/10/331,053
; CURRENT FILING DATE: 2002-12-26
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 70
; LENGTH: 133300
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(133300)
; OTHER INFORMATION: n = A, T, C or G
; US-10-331-053-70

Query Match      36.7%; Score 163.6%; DB 13; Length 912;
Best Local Similarity 82.0%; Pred. No. 1.2e-29;
Matches 187; Conservative 1; Mismatches 40; Indels 0; Gaps 0;

Qy          1 TGCCACGATCTCGTCACTGAACTCCAGTAGCTGGATTACAGC 64
Db          39 TGCAGGTCAAGCACTCTCTCCATGCTTCAGCTGGATTACGGATG 98
Qy          5 TGCCACGATCTCGTCACTGAACTCCAGTAGCTGGATTACAGC 64
Db          39 TGCAGGTCAAGCACTCTCTCCATGCTTCAGCTGGATTACGGATG 98
Qy          65 GCCACCAAGCCCGCTTAATTCTGATCTTTAGTAGAGACGGCTTCCATGTTGTC 124
Db          99 GCCACCAAGCCCGCTTAATTCTGATCTTTAGTAGAGACGGCTTCCATGTTGTC 158
Qy          125 AGGCTGGCTCTCABAATCTCAGTGATCCGGCTCGCCCTCCAAAGTCTA 184
Db          159 AGGCTAGTCGAATCCAACTCAAGTCGATCCAGTCGCTCCAAAGTCTA 218
Qy          185 GGATTAAGGGTAGGCAAGCGGCTAGCCCTGGAAACCTTTCTT 232
Db          219 GGATTAAGGGTAGGCAAGCGGCTAGCCCTGGAAACCTTTCTT 266

RESULT 10
; Sequence 165143, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827-129
; CURRENT APPLICATION NUMBER: US/10/027 632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,066
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,052
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: abcSEQ for Windows Version 4.0
; SEQ ID NO 165143
; LENGTH: 912
; TYPE: DNA
; ORGANISM: Human
; US-10-027-632-165143

Query Match      36.7%; Score 163.6%; DB 13; Length 912;
Best Local Similarity 82.0%; Pred. No. 1.2e-29;
Matches 187; Conservative 1; Mismatches 40; Indels 0; Gaps 0;

Qy          1 TGCCACGATCTCGTCACTGAACTCCAGTAGCTGGATTACAGC 64
Db          39 TGCAGGTCAAGCACTCTCTCCATGCTTCAGCTGGATTACGGATG 98
Qy          5 TGCCACGATCTCGTCACTGAACTCCAGTAGCTGGATTACAGC 64
Db          39 TGCAGGTCAAGCACTCTCTCCATGCTTCAGCTGGATTACGGATG 98
Qy          65 GCCACCAAGCCCGCTTAATTCTGATCTTTAGTAGAGACGGCTTCCATGTTGTC 124
Db          99 GCCACCAAGCCCGCTTAATTCTGATCTTTAGTAGAGACGGCTTCCATGTTGTC 158

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Qy 125 AGGCTGGTCGAACCTCAACCTCAGGTATCCGCCGCCTCGCCCTCCAAAGTGCATA 184  
 Db 159 AGGCTAGTCGAACCTCCACCTCTGATCCGGCTCAGCTCCAAAGTGCATA 218

Qy 185 GGATTACAGGGGTGAGCACCGGGCTCAAGCTGGAAACACCTTTCTT 232  
 Db 219 GGATTACAGGGTGACACTGCGCCAGCTGGTGGACCATTT 266

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RESULT 11  
 US-10-027-632-165142  
*; Sequence 165142, Application US/10027632*  
*; Publication No. US20030204075A9*  
*; GENERAL INFORMATION:*  
*; APPLICANT: Wang, David G.*  
*; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide*  
*; Polymorphisms in the Human Genome*  
*; FILE REFERENCE: 108827.129*  
*; CURRENT FILING DATE: 2002-04-10*  
*; PRIORITY APPLICATION NUMBER: US 10/027,632*  
*; CURRENT FILING DATE: 2002-04-10*  
*; PRIORITY APPLICATION NUMBER: US 60/218,006*  
*; PRIORITY APPLICATION NUMBER: US 60/198,676*  
*; PRIORITY APPLICATION NUMBER: US 60/193,483*  
*; PRIORITY APPLICATION NUMBER: US 60/185,218*  
*; PRIORITY APPLICATION NUMBER: US 60/146,002*  
*; PRIORITY APPLICATION NUMBER: US 60/146,002*  
*; PRIORITY APPLICATION NUMBER: US 60/167,363*  
*; PRIORITY APPLICATION NUMBER: US 60/156,358*  
*; PRIORITY APPLICATION NUMBER: US 60/156,358*  
*; PRIORITY APPLICATION NUMBER: US 60/198,676*  
*; PRIORITY APPLICATION NUMBER: US 60/193,483*  
*; PRIORITY APPLICATION NUMBER: US 60/185,218*  
*; PRIORITY APPLICATION NUMBER: US 60/146,002*  
*; PRIORITY APPLICATION NUMBER: US 60/146,002*  
*; NUMBER OF SEQ ID NOS: 325720*  
*; SOFTWARE: FastSEQ for Windows Version 4.0*  
*; SEQ ID NO: 165142*  
*; LENGTH: 912*  
*; TYPE: DNA*  
*; ORGANISM: Human*  
*; US-10-027-632-165143*

Query Match 36.7%; Score 163.6; DB 15; Length 912;  
 Best Local Similarity 82.0%; Pred. No. 1.2e-29; Indels 0; Gaps 0;  
 Matches 187; Conservative 1; Mismatches 40; Indels 0; Gaps 0;

Qy 5 TGGCAGCATTCGTCACTGCAACTCAGCTCCAGTAGCTGGATTACAGGCATGC 64  
 Db 39 TGCCAGGTCAAGGACTTCCTCGCTCAGCTCCAGTAGCTGGATTACAGGCATG 98

Qy 65 GCCAACCCAGCCCCGGCTAAATTGTATCTTTAGTAGAGGGCTTCATGGTGGTC 124  
 Db 99 GCAACACGGCTGGTTATTGTATTTAGTAGAKACGGGGTTCTCATGGTGGTC 158

Qy 125 AGGGCTGGTCGAACCTCAACCTCAGGTATCCGCCCTCGCCCTCCAAAGTGCATA 184  
 Db 159 AGGCTAGTCGAACCTCCACCTCTGATCCGGGTTTCATGGTGGCTC 218

Qy 185 GGATTACAGGGGTGAGCACCGGGCTCAAGCTGGAAACACCTTTCTT 232  
 Db 219 GGATTACAGGGTGACACTGCGCCAGCTGGTGGACCATTT 266

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RESULT 12  
 US-10-027-632-165143  
*; Sequence 165143, Application US/10027632*  
*; Publication No. US20030204075A9*  
*; GENERAL INFORMATION:*  
*; APPLICANT: Wang, David G.*  
*; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide*  
*; Polymorphisms in the Human Genome*  
*; FILE REFERENCE: 108827.129*

		OTHER INFORMATION: "n" at positions 13303 to 21086 can be any base
FEATURE:		
NAME/KEY:	misc_feature	
LOCATION:	(30979)..(31963)	
OTHER INFORMATION:	"n" at positions 30929 to 31963 can be any base	
US-10-052-482-226		
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		Best Local Similarity      87.6%;    Pred. No. 9.5e-29;
		Matches 190;    Conservative 0;    Mismatches 26;    Indels 1;    Gaps
Qy	1	GTAATGGACGATCTCGTCACTGAAACCTGAGCTCCCGAGTCCTGGATTACAA
Ddb	76411	GC GTGGGTGATCTCGCTACTGAACTCCGGAGTCCTGGATTACAA
Qy	61	ATCGCACCACCCCCGCTTAATTCTATCTTTAGTAGACGCGTCTCCAT
Ddb	76411	ATGCACACACGCCCGCTAATTGA - ATTITAGTAGATGGTTGGCTCCAA
Qy	121	GCTCAGGTGGTCTCGAACCTCAAACCTCAAGTGATCAGCCGCTCGGGCTCCAA
Ddb	76510	GCCAAAGGGTGTGAACTCCAAACCTCAAGTGATCAGCCGCTCGGGCTCCAA
Qy	181	GCTTGGATTACGGGTGAGCCACGGCTCAGCTG 217
Ddb	76590	GCTGGGGTTACGGCATAGCCACCGGGCCCTG 76626

Qy	143	AAACCTTCAGGTGTATCGCCGCTCGGCCCTCCAAAGTCAGGTTACAGGGTGAGCC	202
Db	298	CAACCTTCAGGTGTATCGCCGCTCGGCCCTCCAAAGTCAGGTTACAGGGTGAGCC	239
Qy	203	ACCGCGCTCAAGCTGGAAACACCTTCTTACATCTCAAGTGTCAAATGTTATGAA	262
Db	238	ACCGCGCTGGCTCAACTACCCCTTCTCATTAAGATGAAACATTAATTATGAA	179
Qy	263	AACGAAGAAAGATTATAAGGTAAATTATAAGAACACTATTCTTCCAAAGAG	322
Db	178	AAATAATATGGATGTATGGGGAGGAGAATGGTAGCTCATGTGAAAGTGTAAA	119
Qy	323	CCAAGATTCTCTTCTCTCTTCTTTTTT	357
Db	118	CCAGCAGATAAAATAAGACATGTCATCTATGTT	84
RESULT 15			
	US-10-027-632-117278/C		
	Sequence 117278, Application US/100277632		
	Publication No. US2020198371A1		
	GENERAL INFORMATION:		
	APPLICANT: Wang, David G.		
	TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome		
	FILE REFERENCE: 108827.129		
	CURRENT APPLICATION NUMBER: US/10/027,632		
	CURRENT FILING DATE: 2002-04-30		
	PRIOR APPLICATION NUMBER: US 60/218,006		
	PRIOR FILING DATE: 2000-07-12		
	PRIOR APPLICATION NUMBER: US 60/198,676		
	PRIOR FILING DATE: 2000-04-20		
	PRIOR APPLICATION NUMBER: US 60/193,483		
	PRIOR FILING DATE: 2000-03-29		
	PRIOR APPLICATION NUMBER: US 60/185,218		
	PRIOR FILING DATE: 2000-02-24		
	PRIOR APPLICATION NUMBER: US 60/167,163		
	PRIOR FILING DATE: 1999-11-12		
	PRIOR APPLICATION NUMBER: US 60/156,358		
	PRIOR FILING DATE: 1999-09-28		
	PRIOR APPLICATION NUMBER: US 60/146,002		
	PRIOR FILING DATE: 1999-08-09		
	NUMBER OF SEQ ID NOS: 325720		
	SOFTWARE: FASTSEQ For Windows Version 4.0		
	SEQ ID NO: 112278		
	LENGTH: 1136		
	TYPE: DNA		
	ORGANISM: Human		
	US-10-027-632-117278		
Qy	3	Query Match Score 163; DB 13; Length 1136;	
	Best Local Similarity Pred. No. 1.8e-39;		
	Matches 226; Conservative 2; Mismatches 107; Indels 0; Gaps 0;		
Qy	23	CTGCAACCTCAAGCTCCAGTAGCTGGATTACAGGCATGGCCACCAGCGCCGGCTAA	82
Db	418	CTCCCTGCCTCAGCCTCTGAGTAGCTGGATTACAGCATGACCCCAAGCGCCGGCTAA	359
Qy	83	TTTTGTATCTTGTAGTAGAGACGGCTTCCTCCATTTGCTCAGGAACCTTC	142
Db	358	TTTTGTATCTTGTAGTAGYGGGTTTACCATCTGGTCAAGCTGGTCTGGTAACTCC	299
Qy	143	AAACCTTCAAGCTGGAAACACCTTCTCTTCAAGTGTCAAATGTTATGAA	202
Db	298	CAACCTTCAAGCTGGAAACACCTTCTCTTCAAGTGTCAAATGTTATGAA	239
Qy	203	ACCGCGCTCAAGCTGGAAACACCTTCTCTTCAAGTGTCAAATGTTATGAA	262
Db	238	ACCGCGCTGGCTCACTACCCCTTCTCTTCAAGTGTCAAATGTTATGAA	179
Qy	263	AACGAAGAAAGATTATAAGAGTAAATTATAAGAACACTTCTTCCAAAGAG	322
Db	178	AAATAATATGGCTCATGGGGAGGAGAATGGTAGCTCATGTGAAAGTGTAAA	119

Qy        323 CCAAGATTCCTCTTCTCTCTCTTTTTTT 357  
          ||| | | | | | | | | | | | | | | | | |  
Db        118 CCAGCAGATAAAATAGACATGCTATCTATGTT 84

Search completed: January 15, 2005, 19:18:03  
Job time : 392 secs

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ORIGIN		Matches	179; Conservative	0; Mismatches	30;	Indels	0;	Gaps	0;
Query Match	Score 161.4; DB 5; Length 660;	QY	23	CTGCAACCTCAGCCTCCCCAGTAGCTGGATTACAGGCATGGCCACCAAGGCCCTAA	82				
Best Local Similarity	76.4%; Fred. No. 4.8e-18;		Db	111	CTCCCTGCCCTGCCCTCCAGCTGGATTACAGGCATGGCCACCAAGGCCCTAA	151			
Matches	198; Conservative 0; Mismatches 61;								
QY	23 CTGCAACCTCAGCCTCCCCAGTAGCTGGATTACAGGCATGGCCACCAAGGCCCTAA 82	QY	83	TTTTGTATCTTGTAGTAGAGCAGCGGTTCCTCATGTTGGCTGGCTGGATTATAGGCATGTGCCAACGCCCTAA	142				
Db	111 CTCCCTGCCCTGCCCTCCAGCTGGATTACAGGCATGGCCACCAAGGCCCTAA 170	Db	152	TTTGTATTTGTAGCTGGATTATAGGCATGTGCCAACGCCCTAA	211				
QY	83 TTTTGTATCTTGTAGTAGAGCAGCGGTTCCTCATGTTGGCTGGATTATAGGCATGTGCCAACGCCCTAA 142	QY	143	AAACTCTAGGTGATCGCCGCCCTGCCCTGGAAACACCTTTCT	202				
Db	171 TTGTATTTGTAGAGCAGCGGTTCCTCATGTTGGCTGGATTATAGGCATGTGCCAACGCCCTAA 230	Db	212	CGACCTAGGTGATCGCCGCCCTGGAAACACCTTTCT	271				
QY	143 AAACCTCTAGGTGATCGCCGCCCTGCCCTGGAAACACCTTTCT	QY	203	ACGGCGCTCACGGCTGGAAACACCTTTCT	231				
Db	231 CAACCTCTAGGTGATCGCCGCCCTGGAAACACCTTTCT	Db	272	ACCGCGCTCACGGCTGGAAACACCTTTCT	300				
QY	203 ACGGCGCTCACGGCTGGAAACACCTTTCT	RESULT 5	AQ419825	LOCUS	RPCI-11-179F14-TJ	624 bp	DNA	linear	GSS 23-MAR-1999
Db	291 ACTGGGCCAACCTTAATGGTTTGTGTTATAAACCGGACTCTGAATGTCATCAA 350	DEFINITION	AQ419825	DEFINITION	RPCI-11-179F14				Genomic survey sequence.
QY	263 AACGAAAAAAGAAATTAA 281	ACCESSION	AQ419825	ACCESSION	AQ419825				
Db	351 TAATTCAAATATTATA 369	KEYWORDS	GSS.	KEYWORDS	GSS.				
RESULTS 4		ORGANISM	Homo sapiens (human)	ORGANISM	Homo sapiens				
LOCUS	BE464585	COMMENT	Unpublished (1997)	COMMENT	Other GSSs: RPCI-11-179F14-TV				
DEFINITION	hs85a05_x1 NCI CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3143984_3, similar to conTains_Alu repetitive element;, mRNA sequence.	REFERENCE	1 (bases 1 to 624)	REFERENCE	Contact: Shaying Zhao, William Nierman, Mark Adams				
ACCESSION	BE464585	AUTHORS	Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter,J.C.	AUTHORS	Department of Eukaryotic Genomics				
VERSION	BE464585.1	TITLE	USE of BAC End Sequences from Library RPCI-11 for Sequence-Ready Map Building	TITLE	The Institute for Genomic Research				
KEYWORDS	EST,	SOURCE	9712 Medical Center Dr., Rockville, MD 20850	SOURCE	9712 Medical Center Dr., Rockville, MD 20850				
SOURCE		ORGANISM	Homo sapiens	ORGANISM	Unpublished (1997)				
ORGANISM		COMMENT	Email: hb@tigr.org	COMMENT	Other GSSs: RPCI-11-179F14-TV				
BE464585	BE464585	DEFINITION	Copies are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@jong.med.buffalo.edu). Clones may be purchased from BACPAC Resources ( <a href="http://bacpac.med.buffalo.edu/ordering">http://bacpac.med.buffalo.edu/ordering</a> ) or from Research Genet cs (info@resgen.com). BAC end search page: <a href="http://www.tigr.org/cdb/humgen/bac_end_search.html">http://www.tigr.org/cdb/humgen/bac_end_search.html</a> .	DEFINITION	Contact: Shaying Zhao, William Nierman, Mark Adams				
hs85a05_x1 NCI CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3143984_3, similar to conTains_Alu repetitive element;, mRNA sequence.	REFERENCE	REFERENCE	1 (bases 1 to 624)	REFERENCE	Department of Eukaryotic Genomics				
ACCESSION	BE464585	AUTHORS	Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter,J.C.	AUTHORS	The Institute for Genomic Research				
VERSION	BE464585.1	TITLE	USE of BAC End Sequences from Library RPCI-11 for Sequence-Ready Map Building	TITLE	9712 Medical Center Dr., Rockville, MD 20850				
KEYWORDS	EST,	SOURCE	Tel: 301 838 0200	SOURCE	Unpublished (1997)				
SOURCE		ORGANISM	Homo sapiens	ORGANISM	Unpublished (1997)				
ORGANISM		COMMENT	Fax: 301 838 0208	COMMENT	Other GSSs: RPCI-11-179F14-TV				
BE464585	BE464585	DEFINITION	Email: hb@tigr.org	DEFINITION	Contact: Shaying Zhao, William Nierman, Mark Adams				
hs85a05_x1 NCI CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3143984_3, similar to conTains_Alu repetitive element;, mRNA sequence.	REFERENCE	REFERENCE	Copies are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@jong.med.buffalo.edu). Clones may be purchased from BACPAC Resources ( <a href="http://bacpac.med.buffalo.edu/ordering">http://bacpac.med.buffalo.edu/ordering</a> ) or from Research Genet cs (info@resgen.com). BAC end search page: <a href="http://www.tigr.org/cdb/humgen/bac_end_search.html">http://www.tigr.org/cdb/humgen/bac_end_search.html</a> .	DEFINITION	Contact: Shaying Zhao, William Nierman, Mark Adams				
ACCESSION	BE464585	AUTHORS	Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter,J.C.	AUTHORS	Department of Eukaryotic Genomics				
VERSION	BE464585.1	TITLE	USE of BAC End Sequences from Library RPCI-11 for Sequence-Ready Map Building	TITLE	The Institute for Genomic Research				
KEYWORDS	EST,	SOURCE	9712 Medical Center Dr., Rockville, MD 20850	SOURCE	Unpublished (1997)				
SOURCE		ORGANISM	Homo sapiens	ORGANISM	Unpublished (1997)				
ORGANISM		COMMENT	Tel: 301 838 0200	COMMENT	Other GSSs: RPCI-11-179F14-TV				
BE464585	BE464585	DEFINITION	Fax: 301 838 0208	DEFINITION	Contact: Shaying Zhao, William Nierman, Mark Adams				
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REFERENCE		AUTHORS	Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter,J.C.	AUTHORS	The Institute for Genomic Research				
ACCESSION	BE464585	TITLE	USE of BAC End Sequences from Library RPCI-11 for Sequence-Ready Map Building	TITLE	9712 Medical Center Dr., Rockville, MD 20850				
VERSION	BE464585.1	KEYWORDS	Tumor Gene Index	KEYWORDS	Unpublished (1997)				
KEYWORDS		SOURCE	Unpublished (1997)	SOURCE	Unpublished (1997)				
SOURCE		ORGANISM	Homo sapiens	ORGANISM	Unpublished (1997)				
ORGANISM		COMMENT	Contact: Robert Straussberg, Ph.D.	COMMENT	Other GSSs: RPCI-11-179F14-TV				
BE464585	BE464585	DEFINITION	Email: cgapb-r@mail.nih.gov	DEFINITION	Contact: Robert Straussberg, Ph.D.				
hs85a05_x1 NCI CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3143984_3, similar to conTains_Alu repetitive element;, mRNA sequence.	REFERENCE	REFERENCE	Tissue Procurement: Chris Moskaluk, M.D., Michael R. Emmert-Buck, M.D., Ph.D. DNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: Christa Orange, The I.M.A.G.E. Consortium DNA Sequencing by: Washington University Genome Sequencing Center	REFERENCE	Email: cgapb-r@mail.nih.gov				
REFERENCE		AUTHORS	Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LIULN, send email to: info@image.IIULN.gov	AUTHORS	Tissue Procurement: Chris Moskaluk, M.D., Michael R. Emmert-Buck, M.D., Ph.D. DNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: Christa Orange, The I.M.A.G.E. Consortium DNA Sequencing by: Washington University Genome Sequencing Center				
ACCESSION	BE464585	TITLE	Seq primer: -40UP from Gibco High quality sequence stop: 438.	TITLE	Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LIULN, send email to: info@image.IIULN.gov				
VERSION	BE464585.1	KEYWORDS		KEYWORDS					
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BE464585	BE464585	DEFINITION	Contact: Robert Straussberg, Ph.D.	DEFINITION	Other GSSs: RPCI-11-179F14-TV				
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ORGANISM		COMMENT		COMMENT					
BE464585	BE464585	DEFINITION	Contact: Robert Straussberg, Ph.D.	DEFINITION	Other GSSs: RPCI-11-179F14-TV</				

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Qy	83	TTCCTGATCTTGTAGAGAGCCGTTCCTCCATTTGGTAGGGTCTCGAAGTC	142	Qy	83	TTCCTGATCTTGTAGAGAGCCGTTCCTCCATTTGGTAGGGTCTCGAAGTC	142
Db	265	TTCCTGATCTTGTAGAGATGGATGGAATTCGCTCCATTTGGCTTGACTCC	324	Db	154	TTCCTGATCTTGTAGAGATGGATGGAATTCGCTCCATTTGGCTTGACTCC	212
Qy	143	AAACCTCAGGTGATCCCGCTCGCCCTCCAAAGTGTAGGATTACAGCGTGAAGCC	202	Qy	143	AAACCTCAGGTGATCCCGCTCGCCCTCCAAAGTGTAGGATTACAGCGTGAAGCC	202
Db	325	TGACCTCTAGGTGATCCCGCTCGCCCTCCAAAGTGTAGGATTACAGCGTGAAGCC	384	Db	213	CAACCTCAGGTGATCCCGCTCGCCCTCCAAAGTGTAGGATTACAGCGTGAAGCC	272
Qy	203	ACCGGGCTCAGCTGGAAACACCTTCTTACATCTTCAAGTGTAAATGTTAA	262	Qy	203	ACCCGGCTCAGCTGGAAACACCTTCTTACATCTTCAAGTGTAAATGTTAA	247
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Qy	263	AACGAAAAAGATT	277				
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		DEFINITION					
		392 bp mRNA					
		linear EST 03-PFB-1999					
		IMAGE:1929024 3' Similar to Contains Alu repetitive element, mRNA sequence					
		EST.					
		AI889177					
		KEYWORDS					
		Homo sapiens (human)					
		ORGANISM					
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.					
		REFERENCE					
		AI889177					
		AUTHORS					
		Emmert-Buck, M.D., Ph.D., Michael R.					
		TITLE					
		Unpublished (1997)					
		JOURNAL					
		COMMENT					
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		Homo sapiens					
		ORGANISM					
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		ORGANISM					
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		This clone is available royalty-free through LInL ; contact the IMAGE Consortium (infoimage.lnl.gov) for further information.					
		DEFINITION					
		392 bp mRNA					
		linear EST 03-PFB-1999					
		IMAGE:1929024 3' Similar to Contains Alu repetitive element, mRNA sequence					
		EST.					
		AI889177					
		KEYWORDS					
		Homo sapiens					
		ORGANISM					
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.					
		REFERENCE					
		AI889177					
		AUTHORS					
		Emmert-Buck, M.D., Ph.D., Michael R.					
		TITLE					
		Unpublished (1997)					
		JOURNAL					
		COMMENT					
		Contact: Robert Straubberg, Ph.D.					
		Email: cgsabbs-r@mail.nih.gov					
		This clone is available royalty-free through LInL ; contact the IMAGE Consortium (infoimage.lnl.gov) for further information.					
		DEFINITION					
		392 bp mRNA					
		linear EST 03-PFB-1999					
		IMAGE:1929024 3' Similar to Contains Alu repetitive element, mRNA sequence					
		EST.					
		AI889177					
		KEYWORDS					
		Homo sapiens					
		ORGANISM					
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.					
		REFERENCE					
		AI889177					
		AUTHORS					
		Emmert-Buck, M.D., Ph.D., Michael R.					
		TITLE					
		Unpublished (1997)					
		JOURNAL					
		COMMENT					
		Contact: Robert Straubberg, Ph.D.					
		Email: cgsabbs-r@mail.nih.gov					
		This clone is available royalty-free through LInL ; contact the IMAGE Consortium (infoimage.lnl.gov) for further information.					
		DEFINITION					
		392 bp mRNA					
		linear EST 03-PFB-1999					
		IMAGE:1929024 3' Similar to Contains Alu repetitive element, mRNA sequence					
		EST.					
		AI889177					
		KEYWORDS					
		Homo sapiens					
		ORGANISM					
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.					
		REFERENCE					
		AI889177					
		AUTHORS					
		Emmert-Buck, M.D., Ph.D., Michael R.					
		TITLE					
		Unpublished (1997)					
		JOURNAL					
		COMMENT					
		Contact: Robert Straubberg, Ph.D.					
		Email: cgsabbs-r@mail.nih.gov					
		This clone is available royalty-free through LInL ; contact the IMAGE Consortium (infoimage.lnl.gov) for further information.					
		DEFINITION					
		392 bp mRNA					
		linear EST 03-PFB-1999					
		IMAGE:1929024 3' Similar to Contains Alu repetitive element, mRNA sequence					
		EST.					
		AI889177					
		KEYWORDS					
		Homo sapiens					
		ORGANISM					
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.					
		REFERENCE					
		AI889177					
		AUTHORS					
		Emmert-Buck, M.D., Ph.D., Michael R.					
		TITLE					
		Unpublished (1997)					
		JOURNAL					
		COMMENT					
		Contact: Robert Straubberg, Ph.D.					
		Email: cgsabbs-r@mail.nih.gov					
		This clone is available royalty-free through LInL ; contact the IMAGE Consortium (infoimage.lnl.gov) for further information.					
		DEFINITION					
		392 bp mRNA					
		linear EST 03-PFB-1999					
		IMAGE:1929024 3' Similar to Contains Alu repetitive element, mRNA sequence					
		EST.					
		AI889177			</		

Qy 143 AACCTCTAAGGTGATCCGCCCTCCAAAGTGTAGGATTACAGGGTGAAGC 202  
 Db 217 CAACCTCTAAGGTGATCCGCCCTCCAAAGTGTAGGATTACAGGGTGAAGC 276

Qy 203 ACCGGCTCACCTGGATTACAGGGTCAACTTCAAGTGT 247  
 Db 277 ACCACGCCAGCTTGTTCTTCAGCTCCCTCCAGTACT 321

RESULT 8  
 LOCUS BF790866 467 bp mRNA linear EST 12-JAN-2001  
 DEFINITION 60250663P1 NIH\_MGC\_81 Homo sapiens cDNA clone IMAGE:4338231 5', mRNA sequence.

VERSION BF790866.1 GI:12095920  
 KEYWORDS EST.  
 SOURCE HOME sapiens (human)

ORGANISM Homo sapiens (human)  
 Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1. (bases 1 to 529)  
 AUTHORS Wistow,G.J., Bernstein,S., Behal,A. and Smith,D.  
 TITLE NEIBANK: EST analysis and bioinformatics for ocular genomics  
 JOURNAL Invest. Ophthalmol. Vis. Sci. 41 (2000) In press  
 COMMENT Contact: Wistow G  
 National Eye Institute  
 6/331, NIH, Bethesda, MD 20892-2740, USA  
 Tel: 301 402 3452  
 Fax: 301 496 0078  
 Email: Graeme@helix.nih.gov  
 Plate: 16 a column: 01  
 Seq primer: M13RPI reverse primer (ABI).  
 Location/Qualifiers

FEATURES source  
 1. .529  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="bx16a01"  
 /tissue\_type="Iris"  
 /dev\_stage="Adult"  
 /lab\_host="ENDH10B"  
 /clone\_lib="Human Iris cDNA (un-normalized, unamplified): BX"

/note="Organ: Eye; Vector: PCMVSPORT6; Post-mortem iris tissue was pooled from 10 individuals ranging in age from 4-80 years and RNA was extracted. From this pooled sample an aliquot of 60ug of total RNA yielded 2.17ug of mRNA. A directionally cloned cDNA library in the PCMVSPORT6 vector was constructed at Life Technologies, essentially following the protocols of the SuperScript Plasmid System full details of which are contained in the manufacturer's instruction manual (<http://www.lifetech.com/>). First strand synthesis was carried out using a Not I primer-adaptor (5'-pGACTAGTCTAATGCGAGCGCGCC (T)15-3'). Not I/blunt end inserts were cloned into the Not I/EcoR V sites in the vector. EST analysis was performed on the unamplified library at the NIH Intramural Sequencing Center (NISC)."

ORIGIN

Query Match 35.9%; Score 160.2; DB 2; Length 467;  
 Best Local Similarity 84.9%; Pred. No. 8.4e-18;  
 Matches 191; Conservative 0; Mismatches 33; Indels 1; Gaps 1;

Qy 23 CTGCAACCTCACGCCCTCCCACTAGCTGGATTACAGCATGCCAACAGGCCGCTAA 82  
 Db 342 CTCCCTGCTCACCTCCCTCCGACTAGCTGGATTACAGCATGCCAACAGGCCGCTAA 283

Qy 83 TTTGTTATCTTTAGTAGAGACGGCTTCCNCATATGGCTGGTTCTGCAACTTC 142  
 Db 282 TTTGTTAT-TTTTATGTAAGAGACGGGTTTCTCATGTTGTCAAAGTGGTCTCAACTCC 224

Qy 143 AAACCTCTAAGGTGATCCGCCCTCCAAAGTGTAGGATTACAGGGCTGAGGCC 202  
 Db 223 CAACCTCTAAGGTGATCCAACTTCCCTCCAGTGGGATTACAGGGCTGAGGCC 164

Query Match 35.9%; Score 160.2; DB 2; Length 529;  
 Best Local Similarity 84.9%; Pred. No. 8.2e-18;  
 Matches 191; Conservative 0; Mismatches 33; Indels 1; Gaps 1;

Qy 23 CTGCAACCTCACCTCCGACTAGCTGGATTACAGCATGCCAACAGGCCGCTAA 82  
 Db 331 CTCTGCTCACCTCCCTCCGACTAGCTGGATTACAGCATGCCAACAGGCCGCTAA 272

Qy 83 TTTGTTATCTTTAGTAGAGACGGCTTCCNCATATGGCTGGTTCTGCAACTTC 142  
 Db 271 TTTGTTAT-TTTTATGTAAGAGACGGGTTTCTCATGTTGTCAAAGTGGTCTCAACTCC 213

Qy 143 AAACCTCTAAGGTGATCCGCCCTCCAAAGTGTAGGATTACAGGGCTGAGGCC 202  
 Db 212 CARCTCTAAGGTGATCCAACTTCCCTCCAGTGGGATTACAGGGCTGAGGCC 153

Qy	203	ACCGGCTAGCCCTGGAAACACCTTTCATCTCAAGTGT	247
Db	152	ACACGCCAGCCCTGGTCTTCAGCTCCTCCAGTACT	108
Qy	203	ACCGGCTAGCCCTGGAAACACCTTTCATCTCAAGTGT	247
Db	287	ACACGCCAGCCCTGGTCTTCAGCTCCTCCAGTACT	331
<b>RESULT 1.1</b>			
LOCUS	BM792342	566 bp	mRNA
DEFINITION	UI-HF-BN0-0ff-9-02-0-UI_81 NIH MGC_50 Homo sapiens cDNA clone IMAGE:3066794_3	linear	EST 15-MAR-2000
ACCESSION	AW575808	566	
VERSION	AW575808.1	EST	
KEYWORDS	GI:7247347		
SOURCE	Homo sapiens (human)		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1 (bases 1 to 566)		
AUTHORS	NIH-MGC http://mgc.ncbi.nih.gov/		
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)		
JOURNAL	Unpublished (1999)		
COMMENT	Contact: Robert Strausberg, Ph.D. Email: Cgabbs@medmail.nih.gov		
The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bona fide poly A tail. Tissue Procurement: Louis M. Staudt, M.D., Ph.D.			
CNA Library Preparation: M.B. Soares Lab			
DNA Library Arrayed by: M.B. Soares Lab			
DNA Sequencing by: M.B. Soares Lab			
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/bbcrp/image/image.html			
The following repetitive elements were found in this cDNA sequence:			
10-399, >AUU Seq primer: M13 Forward POLYA:Yes			
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		/db_xref="taxon:9606"	
		/clone_lib="S22SNU16n1"	
		/note="Organ: Stomach; Vector: pT7T3-Pac; Site: 1: ECORI; Site 2: NotI; The S22SNU16 library was contributed by the Soares laboratory and it was constructed as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996). Genome Research 6(9): 791-806. RNA was prepared from harvested cells of SNU-16 culture. SNU-16 cell was obtained from Korean Cell Line Bank (KCLB). SNU-16 was established from ascitic fluids of Korean patients by Park J.G. et al. (1990), Cancer Res 50: 2773-2780."	
		/cell_line="SNU-16"	
		/lab_host="DH10B"	
		/note="Vector: pT7T3-Pac; Site: 1: Eco RI; Site 2: NotI; The S22SNU16 library was contributed by the Soares laboratory and it was constructed as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996). Genome Research 6(9): 791-806. RNA was prepared from harvested cells of SNU-16 culture. SNU-16 cell was obtained from Korean Cell Line Bank (KCLB). SNU-16 was established from ascitic fluids of Korean patients by Park J.G. et al. (1990), Cancer Res 50: 2773-2780."	
		/cell_type="Lymphoblast-like"	
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		/note="Taxon:9606"	
		/db_xref="taxon:9606"	
		/clone="S22SNU16n1-13-E09"	
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		/cell_type="Lymphoblast-like"	
		/cell_line="SNU-16"	
		/lab_host="DH10B"	
		/note="Vector: pT7T3-Pac; Site: 1: Eco RI; Site 2: NotI; The S22SNU16 library was contributed by the Soares laboratory and it was constructed as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996). Genome Research 6(9): 791-806. RNA was prepared from harvested cells of SNU-16 culture. SNU-16 cell was obtained from Korean Cell Line Bank (KCLB). SNU-16 was established from ascitic fluids of Korean patients by Park J.G. et al. (1990), Cancer Res 50: 2773-2780."	
		/cell_type="Lymphoblast-like"	
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		/clone_lib="NIH MGC 50"	
		/note="Vector: pT7T3-Pac; Site: 1: NotI; Site 2: Eco RI; Constructed from size fractionated cytoplasmic mRNA (3.5-4.4kbl). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Patima Bonaldo, Ph.D. and M. Bento Soares, Ph.D. "	
		/ORIGIN	
		Query Match Score 160.2; DB 2; Length 684;	
		Best Local Similarity 84.9%; Pred. No. 8.1e-18;	
		Matches 191; Conservative 0; Mismatches 33; Indels 1; Gaps 1;	
Qy	23	CTGCAACCTCAGCCCTCCCAGTAGCTGGATTACAGGATGCCAACAGGCCGGCTAA	82
Db	108	CTCTCTGCTCACCCCTCCGAGTAGCTGGATTACAGGATGCCAACAGGCCGGCTAA	167
Qy	83	TTTTGATCTTTAGTAGAGACGCCGGTCTCCATGTTGCTAGGGATCAGGCTGGTCTCGAACCTTC	142
Db	168	TTTTGTAT-TTTTGTATAGAGACGCCGGTCTCCATGTTGCTAGGGATCAGGCTGGTCTCGAACCTTC	226
Qy	143	AAACCTCAGGATGCCGGCTCGGCTCCAAAAGTGTAGGATTACAGGCTGGACGCC	202
Db	227	CAACCTCAGGATGCCAACCTGCCGGTCTCCAAAAGTGTAGGATTACAGGCTGGACGCC	286
Qy	203	ACCGGGCTAGCCCTGGAAACACCTTTCATCTCAAGTGT	247

Db	260	ACCAAGCCCAGCCTGGGTTCAGCTCCAGTACT 216	KEYWORDS EST. Homo sapiens (human)
RESULT	12		SOURCE Homo sapiens
BIOS	BI087063/c	740 bp mRNA linear EST 20-JUN-2001	ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
LOCUS	602850725F1 NIH_MGC_10	Homo sapiens cDNA clone IMAGE:4992270 5', mRNA sequence.	REFERENCE 1 (bases 1 to 906) NIH-MGC http://mgc.ncbi.nih.gov/
DEFINITION			AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
ACCESSION	BI087063		TITLE Unpublished (1999)
VERSION	BIG087063.1	GI:14505393	JOURNAL Unpublished (1999)
KEYWORDS	EST.		COMMENT Contact: Robert Strausberg, Ph.D. Email: cgabps-r@mail.nih.gov
ORGANISM	Homo sapiens	Homo sapiens (human)	TISSUE Procurement: ATCC
REFERENCE	1 (bases 1 to 740)	NIH-MGC http://mgc.ncbi.nih.gov/	CDNA Library Preparation: Life Technologies, Inc.
AUTHORS		National Institutes of Health, Mammalian Gene Collection (MGC)	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (L1NL)
TITLE		Unpublished (1999)	DNA Sequencing by: Incyte Genomics, Inc.
JOURNAL			Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/L1NL at: http://image.lnl.gov
COMMENT		Contact: Robert Strausberg, Ph.D. Email: cgabps-r@mail.nih.gov	Plate: L1AM1011 row: d column: 19
FEATURES			High quality sequence start: 4 High quality sequence stop: 674.
SOURCE			Location/Qualifiers 1 .906 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="IMAGE:4509282" /tissue_type="embryonal carcinoma, cell line" /lab_host="DH10B (phage-resistant)" /clone_lib="NIH MGC_92"
			/note="Organ: cervix; Vector: pcMV-SPORT6; Site_1: NotI; Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.5 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."
ORIGIN			Query Match Best Local Similarity 35.9%; Score 160.2; DB 4; Length 906; Matches 191; Conservative 0; Mismatches 33; Indels 1; Gaps 1;
			Qy 23 CTGCAACCTAGCTCCAGTAGCTGGATTACAGGATGCGGACCAGGCCGCTAA 82 Db 482 CTCTGCGCTACCTCTCCGAGTACTGGGATTACAGGATGCGGACCAGGCCGCTAA 423
			Qy 83 TTTCATCATTTTACTAGAACGGGTTCTCCATGTTGTCAGCTGCTCGAATTC 142 Db 422 TTTCATAT-TTTTATAGAACGGGTTCTCCATGTTGTCAGCTGCTCGAATTC 364
			Qy 143 AACCTCAGTGTATCGCCGGCTGGCTTCAGGATTCAGGTTACGGGTTACGGGTGAGGCC 202 Db 363 CAACTCAGTGTATCCACCTGGCTGGCTGGCTTCAGGATTCAGGTTACGGGTGAGGCC 304
			Qy 203 ACCGGCTCAAGCTGGAAACCTTTCTCATCTTCAAGTGTCT 247 Db 303 ACCACGCCAGCTGGCTGGTTCTCCAGTGTCTCCAGTACT 259
			RESULT 14 CN426512/C LOCUS CN426512 DEFINITION 1700470665591 GRN_ES Homo sapiens mRNA sequence. ACCESSION CN426512 VERSION EST KEYWORDS Homo sapiens ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 714)		AUTHORS Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J., Li,Y., Xu,C., Fang,R., Guequier,K., Rao,M.S., Mandelam,R., Lebkowski,J and Stanton,L.W.
RESULT	13	AAACCTCAAGCTGATCCGCCCTCCCTGGCTTACAGGCTTACGGCTGAGGCC 202	
LOCUS	BG259634/c	906 bp mRNA linear EST 13-FEB-2001	
DEFINITION	602378774F1 NIH_MGC_92	Homo sapiens cDNA clone IMAGE:4503282 5', mRNA sequence.	
ACCESSION	BG259634		
VERSION	BG259634.1	GI:12769450	

**TITLE** Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation  
**JOURNAL** Natl. Biotechnol. 22 (6), 707-716 (2004)  
**COMMENT** Contact: Brandenberger R  
 Regenerative Medicine  
 Geron Corporation  
 230 Constitution Drive, Menlo Park, CA 94025, USA  
 Tel : 650 473 8658  
 Fax: 650 473 7760  
 Email: rbrandenberger@geron.com  
**FEATURES** Insert Length: 714 Std Error: 0.00.  
**source** Location/Qualifiers 1. "714 /organism="Homo sapiens"  
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 /db\_xref="taxon:9606"  
 /tissue\_type="embryonic stem cells, cell lines H1, H7, and H9"  
 /clone\_lib="GRN\_ES"  
 /note="Oligo dt primed, full-length enriched cDNA library from differentiated hES cell lines H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free conditions"  
**ORIGIN**

Query Match	35.9%; Score 160; DB 7; Length 714;	Qy	89 ATCTTTAGTAGAGACCGCGTTCATGTTGGTCAAGCTGTCTGAACCT 148
Best Local Similarity	74.3%; Pred. No. 8.3e-18;	Qy	1419 TATTITAGAGACGGGTTCTCATGTTGGTCAAGCTGTCTGAACCT 1478
Matches	202; Conservative 0; Mismatches 70; Indels 0; Gaps 0;	Db	1419 TATTITAGAGACGGGTTCTCATGTTGGTCAAGCTGTCTGAACCT 1478

Qy 23 CTGCAACCTCAGCCCTCCAGTAGCTGGATTACAGGCATGCCAACAGCCGGCTAA 82  
 Db 387 CCTCTGCCTCAGCCCTCTGAGTAGGGATTACAGGATGCCACATGCCGAA 328  
 Qy 83 TTTCGTATCTTTAGTAGAGACGGGTCTCCATGTTGGTCAAGCTGTCTGAACCTC 142  
 Db 327 TTTCGTATTTAGTAGAGACGGGTCTACATGTTGGTCAAGCTGTCTGAACCTC 268  
 Qy 143 AAACCTCAGGTGATGCCGCCCTCCAAAGCTGATTAACGGGTGACCC 202  
 Db 267 TGACCTCAGGTGATCACCTGCCCTCCAAATGCTGATTAACGGGTGACCC 208  
 Qy 203 ACCGGCTCAAGCTGGAACACCTTCTTACATCTCAAGTGTAGAA 262  
 Db 207 ACCAGCCGGCTTGATTTAAATCTATAATCTCAATAATAAATGTTTTC 148  
 Qy 263 AACGAAAAAAAGAATTATAAGTAATTATAA 294  
 Db 147 ATGGAAAATGTCCTTTAAATGTAATTAAA 116

Search completed: January 15, 2005, 18:21:48  
 Job time : 2262 sec8

**RESULT 15**  
**CR619941** CR619941 1686 bp mRNA linear HTC 21-JUL-2004  
**DEFINITION** full-length cDNA clone CSODF033Y108 of Fetal brain of Homo sapiens (human).  
**ACCESSION** CR619941  
**VERSION** CR619941.1 GI:50500748  
**KEYWORDS** HTC; CNSLT\_cDNA.  
**ORGANISM** Homo sapiens (human).  
**REFERENCE** 1 (bases 1 to 1686)  
**AUTHORS** Li,W.B., Gruber,C., Jesse,J. and Polayes,D.  
**TITLE** Full-length cDNA Libraries and normalization.  
**JOURNAL** Unpublished  
**REMARK** Contact : Peng Liang Email : Elian@lifetech.com URL : http://fulllength.invitrogen.com/InvitroGen Corporation 1600 Faraday Avenue  
**REFERENCE** 2 (bases 1 to 1686)  
**AUTHORS** Genoscope.  
**TITLE** Direct Submission  
**JOURNAL** Submitted (20-JUL-2004) Genoscope - Centre National de Sequencing : BP 191 91006 EVRY cedex - FRANCE (E-mail : seque@genoscope.cns.fr